

STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-714-741-42

Query Match 22.5%; Score 108; DB 4; Length 588;
Best Local Similarity 29.9%; Pred. No. 0.014;
Matches 32; Conservative 22; Mismatches 33; Indels 20; Gaps 3;

QY 4 YESTQEQIEELKDYNEQISEG--ETILIAIQ-----NKISDLDKIA 44
DB 483 YE-VORLLKELKEIDESDYLYKGLRPLQSLDTKAKLSKLEELSDKIDBLDAIA 541
QY 45 EAEKKLADSQNGEGVEDYWTSGDEKLEKLAQAEQDELQAEQLDQLDE 91
DB 542 KLEVQLKDAEGNNVEAFKSGLEKTTAEKKALEKAEADLKKAUDE 588

RESULT 14
US-09-949-016-6468
Sequence 6468, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6468
LENGTH: 1979
TYPE: PRT
ORGANISM: Human
US-09-949-016-6468

Query Match 22.3%; Score 107; DB 4; Length 1979;
Best Local Similarity 25.6%; Pred. No. 0.085;
Matches 31; Conservative 19; Mismatches 29; Indels 42; Gaps 3;
QY 1 QALVESTQEQIEELKDYNEQISEGETL-----ILAIQ----- 33

DB 245 QKLTISRHRREELSDYEERIEELENLLQGGSGVIETDLSKIYEMQKTIQVLQIEKVES 304
QY 34 -NKISDLDKIAEAEKKLADSQNGEGVEDYWTSGDEKLEKLAQAEQDELQAEQLDQLDE 92
DB 305 TKKMEQLEDKIKDINKKLSAENDRDI-----LRREQSOLNVEKQIWEEC 350
QY 93 D 93
DB 351 E 351

RESULT 15

US-09-949-016-7404
Sequence 7404, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7404
LENGTH: 2047
TYPE: PRT
ORGANISM: Human
US-09-949-016-7404

Query Match 22.3%; Score 107; DB 4; Length 2047;
Best Local Similarity 25.6%; Pred. No. 0.089;
Matches 31; Conservative 19; Mismatches 29; Indels 42; Gaps 3;

QY 1 QALVESTQEQIEELKDYNEQISEGETL-----ILAIQ----- 33
DB 313 QKLTISRHRREELSDYEERIEELENLLQGGSGVIETDLSKIYEMQKTIQVLQIEKVES 372
QY 34 -NKISDLDKIAEAEKKLADSQNGEGVEDYWTSGDEKLEKLAQAEQDELQAEQLDQLDE 92
DB 373 TKKMEQLEDKIKDINKKLSAENDRDI-----LRREQSOLNVEKQIWEEC 418
QY 93 D 93
DB 419 E 419

Search completed: November 17, 2005, 19:32:24
Job time : 18.6081 secs

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match 22.7%; Score 109; DB 2; Length 108;
Best Local Similarity 30.1%; Pred. No. 0.0013;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISLDLDDKIAEAEKKLADSONGEGVEDYWTS 65
Db 21 TQDELD-----KEAAEALNKKVEALPNQVSEELSELSKLELDNLKDAET-NNVEDYIKE 73

Qy 66 GDEKLEKLAQAEQDELQAEQLDQLDEV--DGQE 96
Db 74 GLEEAIAATKQAELEKTPKELDAALNELGPDGDE 106

RESULT 11
US-09-147-875A-23
; Sequence 23, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-23

Query Match 22.7%; Score 109; DB 4; Length 108;
Best Local Similarity 30.1%; Pred. No. 0.0013;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISLDLDDKIAEAEKKLADSONGEGVEDYWTS 65
Db 21 TQDELD-----KEAAEALNKKVEALPNQVSEELSELSKLELDNLKDAET-NNVEDYIKE 73

Qy 66 GDEKLEKLAQAEQDELQAEQLDQLDEV--DGQE 96
Db 74 GLEEAIAATKQAELEKTPKELDAALNELGPDGDE 106

RESULT 12
US-08-529-055-67
; Sequence 67, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.

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; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-67

Query Match 22.7%; Score 109; DB 4; Length 211;
Best Local Similarity 30.1%; Pred. No. 0.0031;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISLDLDDKIAEAEKKLADSONGEGVEDYWTS 65
Db 45 TQDELD-----KEAAEALNKKVEALPNQVSEELSELSKLELDNLKDAET-NNVEDYIKE 97

Qy 66 GDEKLEKLAQAEQDELQAEQLDQLDEV--DGQE 96
Db 98 GLEEAIAATKQAELEKTPKELDAALNELGPDGDE 130

RESULT 13
US-08-714-741-42
; Sequence 42, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.

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Query Match      24.0%; Score 115; DB 4; Length 8991;
Best Local Similarity 29.5%; Pred. No. 0.095;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;

Qy 7 TQEQIEE---LXDYNEQISEGETLILAIQNKISDLDKIAEAKKLADSQNGEGVEDYWT 63
Db 8635 TQDELDKEAAEAELNKEVE-----ALQNQVAELEEELSKLEDNLKDAET-NNVEDYI 8685

Qy 64 TSGDEKLEKLAQDEQLQAEQLDQLLDEV--DGOE 96
Db 8686 KGLEEATATKAELEKTPKELDAALNELGPDGDE 8720

RESULT 8
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-710-749-23

Query Match      22.7%; Score 109; DB 2; Length 108;
Best Local Similarity 30.1%; Pred. No. 0.0013;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISDLDKIAEAKKLADSQNGEGVEDYWT 65
Db 21 TQDELD-----KEAAEAELNKKVEALPNQVSELEELSLEDNLKDAETNH-VEDYIKE 73

Qy 66 GDEKLEKLAQDEQLQAEQLDQLLDEV--DGOE 96
Db 74 GLEEATATKAELEKTPKELDAALNELGPDGDE 106

RESULT 9
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-710-749-23

Query Match      22.7%; Score 109; DB 2; Length 108;
Best Local Similarity 30.1%; Pred. No. 0.0013;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISDLDKIAEAKKLADSQNGEGVEDYWT 65
Db 21 TQDELD-----KEAAEAELNKKVEALPNQVSELEELSLEDNLKDAETNH-VEDYIKE 73

Qy 66 GDEKLEKLAQDEQLQAEQLDQLLDEV--DGOE 96
Db 74 GLEEATATKAELEKTPKELDAALNELGPDGDE 106

RESULT 9
US-08-710-749-23
; Sequence 23, Application US/08710749
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; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-710-749-23

Query Match      22.7%; Score 109; DB 2; Length 108;
Best Local Similarity 30.1%; Pred. No. 0.0013;
Matches 28; Conservative 26; Mismatches 29; Indels 10; Gaps 4;

Qy 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISDLDKIAEAKKLADSQNGEGVEDYWT 65
Db 21 TQDELD-----KEAAEAELNKKVEALPNQVSELEELSLEDNLKDAETNH-VEDYIKE 73

Qy 66 GDEKLEKLAQDEQLQAEQLDQLLDEV--DGOE 96
Db 74 GLEEATATKAELEKTPKELDAALNELGPDGDE 106

RESULT 10
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-70

Query Match 24.0%; Score 115; DB 4; Length 232;
Best Local Similarity 29.5%; Pred. No. 0.0009;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;
QY 7 TOEQIEE---LKDYNQISEGETLILAIQNKISDLDDKIAEAKKLADSQNGEGVEDYW 63
Db 71 TQDELKKAEEAEELNEKVE-----ALQNVAELEELSKELDNLKDAET--NNVEDYI 121
QY 64 TSGDEDKLEKLAQEDELQAEQLDQLDEV--DGQE 96
Db 122 KEGLEEAATKKAELKTKQKELDAALNELGPDGE 156

RESULT 6
US-08-529-055-73
Sequence 73, Application US/08529055
Patent No. 6592876
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESS: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-73
Query Match 24.0%; Score 115; DB 4; Length 458;
Best Local Similarity 29.5%; Pred. No. 0.0021;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;
QY 7 TOEQIEE---LKDYNQISEGETLILAIQNKISDLDDKIAEAKKLADSQNGEGVEDYW 63
Db 296 TQDELKKAEEAEELNEKVE-----ALQNVAELEELSKELDNLKDAET--NNVEDYI 346
QY 64 TSGDEDKLEKLAQEDELQAEQLDQLDEV--DGQE 96
Db 347 KEGLEEAATKKAELKTKQKELDAALNELGPDGE 381
RESULT 7
US-08-714-741-32
Sequence 32, Application US/08714741
Patent No. 6500613
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESS: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-714-741-32

RESULT 5
US-08-529-055-70
; Sequence 70, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; THEREOF, Expression Products
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Thereof, and Uses of Such Genes,
; PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

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OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 18.4831 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-28
Perfect score: 480
Sequence: 1 QALYESTQEQIEELKDYNEQ.....EQDELQAEILDOLLDEVDQGE 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 480 | 100.0 | 96 | 2 | US-08-710-749-28 |
| 2 | 480 | 100.0 | 96 | 4 | US-09-147-875A-28 |
| 3 | 115 | 24.0 | 108 | 2 | US-08-710-749-24 |
| 4 | 115 | 24.0 | 108 | 4 | US-09-147-875A-25 |
| 5 | 115 | 24.0 | 232 | 4 | US-08-529-055-70 |
| 6 | 115 | 24.0 | 458 | 4 | US-08-529-055-73 |
| 7 | 115 | 24.0 | 8991 | 4 | US-08-714-741-32 |
| 8 | 109 | 22.7 | 108 | 2 | US-08-710-749-22 |
| 9 | 109 | 22.7 | 108 | 2 | US-08-710-749-23 |
| 10 | 109 | 22.7 | 108 | 2 | US-08-710-749-26 |
| 11 | 109 | 22.7 | 108 | 4 | US-09-147-875A-23 |
| 12 | 109 | 22.7 | 211 | 4 | US-08-529-055-67 |
| 13 | 108 | 22.5 | 588 | 4 | US-08-714-741-42 |
| 14 | 107 | 22.3 | 1979 | 4 | US-09-949-016-6468 |
| 15 | 107 | 22.3 | 2047 | 4 | US-09-949-016-7404 |
| 16 | 106 | 22.1 | 108 | 4 | US-09-147-875A-24 |
| 17 | 106 | 22.1 | 212 | 4 | US-08-529-055-68 |
| 18 | 105 | 21.9 | 101 | 2 | US-08-710-749-1 |
| 19 | 105 | 21.9 | 1162 | 2 | US-08-728-323A-2 |
| 20 | 105 | 21.9 | 1162 | 3 | US-09-298-568-2 |
| 21 | 105 | 21.9 | 1162 | 4 | US-09-410-399-2 |
| 22 | 105 | 21.9 | 1162 | 4 | US-09-894-273-2 |
| 23 | 104.5 | 21.8 | 1231 | 4 | US-08-714-741-41 |
| 24 | 103.5 | 21.6 | 99 | 4 | US-09-147-875A-16 |
| 25 | 103 | 21.5 | 141 | 4 | US-09-286-981B-2 |
| 26 | 103 | 21.5 | 550 | 4 | US-09-583-110-4871 |
| 27 | 103 | 21.5 | 550 | 4 | US-09-107-433-3858 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 103 | 21.5 | 864 | 4 | US-08-714-741-40 | Sequence 40, Appl |
| 29 | 102.5 | 21.4 | 605 | 4 | US-08-714-741-46 | Sequence 46, Appl |
| 30 | 102 | 21.2 | 101 | 2 | US-08-710-749-2 | Sequence 2, Appl |
| 31 | 102 | 21.2 | 188 | 4 | US-08-529-055-59 | Sequence 59, Appl |
| 32 | 102 | 21.2 | 289 | 1 | US-08-072-070-4 | Sequence 4, Appl |
| 33 | 102 | 21.2 | 289 | 1 | US-08-469-434-4 | Sequence 4, Appl |
| 34 | 102 | 21.2 | 289 | 1 | US-08-214-222-4 | Sequence 4, Appl |
| 35 | 102 | 21.2 | 289 | 2 | US-08-467-852A-5 | Sequence 5, Appl |
| 36 | 102 | 21.2 | 289 | 2 | US-08-468-718-4 | Sequence 4, Appl |
| 37 | 102 | 21.2 | 289 | 2 | US-08-247-491A-5 | Sequence 5, Appl |
| 38 | 100.5 | 20.9 | 99 | 4 | US-09-147-875A-14 | Sequence 14, Appl |
| 39 | 100.5 | 20.9 | 206 | 4 | US-08-529-055-54 | Sequence 54, Appl |
| 40 | 100 | 20.8 | 100 | 4 | US-09-147-875A-2 | Sequence 2, Appl |
| 41 | 99.5 | 20.7 | 99 | 4 | US-09-147-875A-15 | Sequence 15, Appl |
| 42 | 99.5 | 20.7 | 288 | 3 | US-08-312-949-4 | Sequence 4, Appl |
| 43 | 99.5 | 20.7 | 288 | 3 | US-08-446-201-4 | Sequence 4, Appl |
| 44 | 99.5 | 20.7 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |
| 45 | 99.5 | 20.7 | 619 | 1 | US-08-214-164-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-710-749-28
; Sequence 28, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Prommet, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-28

Query Match 100.0%; Score 480; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.2e-40;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QALYESTQEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAEKKLADSQNGEGVE 60
Db 1 QALYESTQEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAEKKLADSQNGEGVE 60

| | | | |
|----|-----|--|-----|
| Db | 224 | SARDEVVELKEQRTLTGQEECL-----RREVOELTDKUSDATHQVAELLEKNQOQNSIDD | 279 |
| Qy | 62 | YWTSGDEDKL--EKLQAEQDELQAEIDQLL | 89 |
| Db | 280 | LSAQLAEQSAIQEKLQAEVNDLRAENDQLL | 309 |

Search completed: November 17, 2005, 20:37:56
Job time : 58.9055 secs

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FT NON_TER 256 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match
Best Local Similarity 23.0%; Score 110.5; DB 2; Length 256;
Matches 35; Conservative 20; Mismatches 27; Indels 23; Gaps 6;

QY 7 TOEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAEKLL-----ADSQNGE--GVE 60
Db 72 TQDELDK-----EAAEDANIEALQNKVADLENKVAELDKVETRLQSLDKAEENNV 123

QY 61 DYTWSGDE----DK---LEKLAQAEQLQAEQLDQLLDEV--DQGE 96
Db 124 DYVKEGLEKALTKKVELNNTQKALDTAQKALDTALNELGPDGDE 168

RESULT 13
Q6BG00
ID Q6BG00 PRELIMINARY; PRT; 2301 AA.
AC Q6BG00;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PTMB.222;
OS Paramécium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramécium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RA PubMed=15296759; DOI=10.1016/j.j.cub.2004.07.029;
RX Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
RA Gromadka R., Noel B.B., Blanc I., Dessen P., Wincker P., Keller A.M.,
RA Cohen J., Meyer E., Sperling L.;
RT "High Coding Density on the Largest Paramécium tetraurelia Somatic
RT Chromosome.";
RL Curr. Biol. 14:1397-1404(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Stock d4-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RT "Paramécium megabase sequencing project.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR548612; CAH03420.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2301 AA; 270852 MW; 41D1B81BFD30F2DF CRC64;

Query Match
Best Local Similarity 22.9%; Score 110; DB 2; Length 2301;
Matches 31; Conservative 21; Mismatches 38; Indels 16; Gaps 2;

QY 7 TOEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAEKLLADSON--GSEGVYWT 65
Db 936 TQENINEKQIQEDITERKNEENNEENNGISNQLDNLQSDKELAEQINVKDSSQISKQ 995

QY 66 GDEKLEKLO-----AEQDELQAEQLDQLLDEVGQE 96
Db 996 GDEQNKETIQENFETEQLOMKGRKEQEQEVNQBEQIESDVRGQE 1041

RESULT 14
Q8IL42
ID Q8IL42 PRELIMINARY; PRT; 3384 AA.
AC Q8IL42;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF14_0407;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255705; PubMed=1236864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.-J., Suh B., Peterson J., Angiuoli S.,
RA Perteau M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014822; AAN37020.1; -.
DR HSSP; P47102; IRE0.
DR InterPro; IPR000904; Sec7.
DR Pfam; PF01369; Sec7; 1.
DR SMART; SM00222; Sec7; 2.
DR PROSITE; PS50190; SEC7; 1.
KW Hypothetical protein.
SQ SEQUENCE 3384 AA; 404580 MW; 340A187BCAEBAG6FD CRC64;

Query Match
Best Local Similarity 22.7%; Score 109; DB 2; Length 3384;
Matches 30; Conservative 18; Mismatches 43; Indels 8; Gaps 1;

QY 5 ESTQEQIEELKDYNEQISEGETLILAIQNKISD-----LDDKIAEAEKLLADSONG 56
Db 3284 DSTQEKEDNIKDSTQDIEDNVDELIEEKQNNIKDSTQEKEDNIKDSTQEKEDNIKDSTQ 3343

QY 57 EGVEDYWTSGDEDKLEKLAQAEQLQAEQLDQLLDEVGQ 95
Db 3344 NKDDNANISNDDEEHEKTKQELKEGKEDDAHSSDEKDGK 3382

RESULT 15
Q7R219
ID Q7R219 PRELIMINARY; PRT; 1024 AA.
AC Q7R219;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 630 79370 82444.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Alley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC Preliminary data.
DR EMBL; AAC01000023; EAA41405.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 9.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 2.
KW ANK repeat.
SQ SEQUENCE 1024 AA; 112846 MW; 7BC6A1926E55BA5F CRC64;

Query Match
Best Local Similarity 22.5%; Score 108; DB 2; Length 1024;
Matches 29; Conservative 25; Mismatches 26; Indels 10; Gaps 4;

QY 6 STQEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAEKLLAD--SONGE--GV 61
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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OX Streptococcus.

RN NCBI_TaxID=1313;

[1] SEQUENCE FROM N.A.

RP STRAIN=SP95;

RX MEDLINE=22241996; PubMed=12354862;

RA Dicunzio G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,

RA Lorino G., Recchia S., Pantosti A., Beall B.;

RT "Genotypes of invasive pneumococcal isolates recently recovered from

RT Italian patients.";

RL J. Clin. Microbiol. 40:3660-3665 (2002).

DR EMBL; AF490265; AAN37733.1; --

FT NON_TER 1

FT NON_TER 211

SQ SEQUENCE 211 AA; 23207 MW; 096BFBEB08CD6483 CRC64;

Query Match 23.1%; Score 111; DB 2; Length 211;

Best Local Similarity 33.3%; Pred. No. 4.4;

Matches 40; Conservative 20; Mismatches 36; Indels 24; Gaps 7;

Qy 1 QALYESTQEQBEL-----KDYNEQISE-GEETLILATONKISDLDKIAEAKKL- 50

Db 2 KAELEKAEAELENLSTLDPEKTOEDLKEAEDVNIEALQNKVADLENKVAELDKVET 61

Qy 51 ---ADSQNGE--GVEDYWTSGDE---DK---LEKLQAEQDELQAEQLDQLLDE--DGOE 96

Db 62 RLQSLDKDAEENNVEDYVKEGLEKALTDKKVELNNTQKALDTAQKALDTALNELGPDGDE 121

RESULT 10

Q9L594

ID Q9L594 PRELIMINARY; PRT; 257 AA.

AC Q9L594;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE PspA (Fragment).

GN Name=pspA;

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus

OX NCBI_TaxID=1313;

[1] SEQUENCE FROM N.A.

RP STRAIN=SP222;

RX MEDLINE=20472698; PubMed=11015380;

RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;

RT "Pneumococcal pspA sequence types of prevalent multiresistant

RT pneumococcal strains in the United States and of internationally

RT disseminated clones.";

RL J. Clin. Microbiol. 38:3663-3669 (2000).

DR EMBL; AF254255; AAF68090.1; --

FT NON_TER 1

FT NON_TER 257

SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 23.1%; Score 111; DB 2; Length 257;

Best Local Similarity 33.3%; Pred. No. 5.4;

Matches 40; Conservative 20; Mismatches 36; Indels 24; Gaps 7;

Qy 1 QALYESTQEQBEL-----KDYNEQISE-GEETLILATONKISDLDKIAEAKKL- 50

Db 48 KAELEKAEAELENLSTLDPEKTOEDLKEAEDVNIEALQNKVADLENKVAELDKVET 107

Qy 51 ---ADSQNGE--GVEDYWTSGDE---DK---LEKLQAEQDELQAEQLDQLLDE--DGOE 96

Db 108 RLQSLDKDAEENNVEDYVKEGLEKALTDKKVELNNTQKALDTAQKALDTALNELGPDGDE 167

RESULT 11,

Q8GNS8

ID Q8GNS8 PRELIMINARY; PRT; 224 AA.

AC Q8GNS8;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE PspA (Fragment).

GN Name=pspA;

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1313;

[1] SEQUENCE FROM N.A.

RP STRAIN=PM124;

RX MEDLINE=22241996; PubMed=12354862;

RA Dicunzio G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,

RA Lorino G., Recchia S., Pantosti A., Beall B.;

RT "Genotypes of invasive pneumococcal isolates recently recovered from

RT Italian patients.";

RL J. Clin. Microbiol. 40:3660-3665 (2002).

DR EMBL; AF490267; AAN37735.1; --

DR HSSP; P00192; IAPC.

DR InterPro; IPR009082; His_kin_homodim.

FT NON_TER 1

FT NON_TER 224

SQ SEQUENCE 224 AA; 23418 MW; 48674E27AFB66A95 CRC64;

Query Match 23.0%; Score 110.5; DB 2; Length 224;

Best Local Similarity 29.3%; Pred. No. 5.1;

Matches 29; Conservative 21; Mismatches 30; Indels 19; Gaps 2;

Qy 12 BELKDYNEQISEG-----BETLILAIQ---NKISDLDKIAEAKKLAD 52

Db 15 QDLKDINESDEYVKEGFRAPLQSELDTKAKLLKLEELSGKTEELDAETAELEVLQKD 74

Qy 53 SONGEGVEDYWTSGDEKLEKLAQEQDELQAEQLDQLLDE 91

Db 75 AEGNNVVEAFKEGLEKTAETAEKAELEKAEADLKKAVIDE 113

RESULT 12

Q9L595

ID Q9L595 PRELIMINARY; PRT; 256 AA.

AC Q9L595;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE PspA (Fragment).

GN Name=pspA;

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1313;

[1] SEQUENCE FROM N.A.

RP STRAIN=SP220;

RX MEDLINE=20472698; PubMed=11015380;

RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;

RT "Pneumococcal pspA sequence types of prevalent multiresistant

RT pneumococcal strains in the United States and of internationally

RT disseminated clones.";

RL J. Clin. Microbiol. 38:3663-3669 (2000).

DR EMBL; AF254254; AAF68089.1; --

FT NON_TER 1

FT NON_TER 256

SQ SEQUENCE 256 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 23.1%; Score 111; DB 2; Length 257;

Best Local Similarity 33.3%; Pred. No. 5.4;

Matches 40; Conservative 20; Mismatches 36; Indels 24; Gaps 7;

Qy 1 QALYESTQEQBEL-----KDYNEQISE-GEETLILATONKISDLDKIAEAKKL- 50

Db 48 KAELEKAEAELENLSTLDPEKTOEDLKEAEDVNIEALQNKVADLENKVAELDKVET 107

Qy 51 ---ADSQNGE--GVEDYWTSGDE---DK---LEKLQAEQDELQAEQLDQLLDE--DGOE 96

Db 108 RLQSLDKDAEENNVEDYVKEGLEKALTDKKVELNNTQKALDTAQKALDTALNELGPDGDE 167

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Matches 30; Conservative 30; Mismatches 35; Indels 15; Gaps 4;
QY 1 QALYESTOQIEEL-----KDYNEQISEGE-ETLILAIONKISLDLDDKIAEAEK 48
Db 49 KAELEKAEAELENLLSTLDPEGKTQDELDKAEAELENKKVQALQNVAELEEEUSKLED 108
QY 49 KLADSONGGEVDYWTSGDEKLEKLAQAEQDELQAEQLDQLDEV--DGOE 96
Db 109 NLKDAET-NNVEDYIKKEGLEEAIAATKAELEKTQKELDAALNELGPDGDE 157

RESULT 6
Q9LAYS
ID Q9LAYS PRELIMINARY; PRT; 426 AA.
AC Q9LAYS;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBL5;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/JAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071810; AAF27706.1; -.
DR HSP; P00192; IMGT.
DR InterPro; IPR011047; Quin_alc_DH_like.
DR InterPro; IPR005333; Tropomyosin.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 426
FT SEQUENCE 426 AA; 46534 MW; 81AAL1348CBE6634 CRC64;

Query Match 23.9%; Score 114.5; DB 2; Length 426;
Best Local Similarity 29.8%; Pred. No. 5.2;
Matches 34; Conservative 21; Mismatches 36; Indels 23; Gaps 3;
QY 1 QALYESTOQIEEL-----EELKDYNEQISEG--ETLILAION-----KIS 37
Db 198 QAKIAELENQVHRLSQDLKDNESDEYVKEGLRPLQSELDYTKAKLLKLELSGKIE 257
QY 38 DLDDKIAEAEKKLADSONGGEVDYWTSGDEKLEKLAQAEQDELQAEQLDQLDE 91
Db 258 ELDAIEALEVQLKDAEGNNVNEAFKEGLEKTTAEKAELEKAEADLKXAVDE 311

RESULT 7
Q8KQK2
ID Q8KQK2 PRELIMINARY; PRT; 107 AA.
AC Q8KQK2;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Pneumococcal surface protein A (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255/00.
RX MEDLINE=22170754; PubMed=12183557;
RX DOI=10.1128/JAI.70.9.5086-5090.2002;
RA Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C.,
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RA Dias W.O., Leite L.C.C.;
RT "Analysis of serum cross-reactivity and cross-protection elicited by
immunization with DNA vaccines against Streptococcus pneumoniae
expressing PspA fragments from different clades.";
RL Infect. Immun. 70:5086-5090(2002).
DR EMBL; AY082390; AAL92495.1; -.
FT NON_TER 1
FT NON_TER 107
FT SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

Query Match 23.8%; Score 114; DB 2; Length 107;
Best Local Similarity 30.1%; Pred. No. 1.4;
Matches 28; Conservative 28; Mismatches 27; Indels 10; Gaps 4;
QY 7 TOEQIEELKDYNEQISEGE-ETLILAIONKISLDLDDKIAEAEKKLADSONGGEVDYWT 65
Db 21 TQDELD-----KEAAEAELENKKVQALQNVAELEEEUSKLEDNLKDAET-NNVEDYIKE 73
QY 66 GDEKLEKLAQAEQDELQAEQLDQLDEV--DGOE 96
Db 74 GLEEAIAATKAELEKTQKELDAALNELGPDGDE 106

RESULT 8
Q8GNS7
ID Q8GNS7 PRELIMINARY; PRT; 213 AA.
AC Q8GNS7;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=128;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicunzio G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490268; AAN37736.1; -.
FT NON_TER 1
FT NON_TER 213
FT SEQUENCE 213 AA; 23490 MW; 23B4428409526EAB CRC64;

Query Match 23.2%; Score 111.5; DB 2; Length 213;
Best Local Similarity 28.6%; Pred. No. 4.1;
Matches 32; Conservative 29; Mismatches 32; Indels 19; Gaps 5;
QY 1 QALYESTOQIEEL-----KDYNEQISEGE-ETLILAIONKISLDLDDKIAEAEK 48
Db 23 KAELEKAEAELENLLSTLDPEGKTQDELDKAEAELENKKVQALQNVAELEEEUSKLED 82
QY 49 --KLADSONGGEVDYWTSGDEKLEKLAQAEQDELQAEQLDQLDEV--DGOE 96
Db 83 NLKVAETNN---VEDYIKKEGLEEAIAATKAELEKTQKALDATALNELGPDGDE 131

RESULT 9
Q8GNT0
ID Q8GNT0 PRELIMINARY; PRT; 211 AA.
AC Q8GNT0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
```

```

RC STRAIN=BG7817;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071826; AAF27719.1; -.
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 479
SQ SEQUENCE 479 AA; 53257 MW; B9C0D2CA15DE3654 CRC64;

Query Match 24.6%; Score 118; DB 2; Length 479;
Best Local Similarity 31.2%; Pred. No. 3.4;
Matches 29; Conservative 27; Mismatches 27; Indels 10; Gaps 4;

QY 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISDLDDKIAEKKLADSONGGEVDYWT 65
Db 315 TQDELD-----KEAAEALNKKVQALQNVAAEELSELSKLEDNLKDAET-NNVEDYI 367

QY 66 GDEKLEKLQARQDELQALDQLDEV--DGQE 96
Db 368 GLEEAIAATKQAELETKQELDAALNELGPDGD 400

RESULT 3
Q9LAX5 PRELIMINARY; PRT; 481 AA.
AC Q9LAX5;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BG11703;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071821; AAF27716.1; -.
DR HSP; P58301; 1L8D.
FT NON_TER 481
SQ SEQUENCE 481 AA; 53500 MW; EA3C66445EFC2B CRC64;

Query Match 24.6%; Score 118; DB 2; Length 481;
Best Local Similarity 31.2%; Pred. No. 3.4;
Matches 29; Conservative 27; Mismatches 27; Indels 10; Gaps 4;

QY 7 TQEQIEELKDYNEQISEGE-ETLILAIQNKISDLDDKIAEKKLADSONGGEVDYWT 65
Db 315 TQDELD-----KEAAEALNKKVQALQNVAAEELSELSKLEDNLKDAET-NNVEDYI 367

QY 66 GDEKLEKLQARQDELQALDQLDEV--DGQE 96
Db 368 GLEEAIAATKQAELETKQELDAALNELGPDGD 400

RESULT 4
O34097 PRELIMINARY; PRT; 653 AA.
AC O34097;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

```

```

DE PspA.
GN Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EF5668;
RX MEDLINE=98427139; PubMed=9746574;
RA McDaniel L.S., McDaniel D.O., Hollingshead S.K., Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
RT to the previously identified PspA sequence from strain Rxi and ability
RT of PspA from EF5668 to elicit protection against pneumococci of
RT different capsular types.";
RL Infect. Immun. 66:4748-4754(1998).
DR EMBL; U89711; AAC62252.1; -.
DR HSP; P06653; 1HCX
DR InterPro; IPR002479; CW binding.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR009053; Prefoldin.
DR Pfam; PF01473; CW binding 1; 9.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
SQ SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

Query Match 24.0%; Score 115; DB 2; Length 653;
Best Local Similarity 29.5%; Pred. No. 7.4;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;

QY 7 TQEQIEE---LKDYNEQISEGEETLILAIQNKISDLDDKIAEKKLADSONGGEVDY 63
Db 296 TQDELDKEAAEALNEKVE-----ALQNVAAEELSELSKLEDNLKDAET-NNVEDYI 346

QY 64 TSGDEKLEKLQARQDELQALDQLDEV--DGQE 96
Db 347 KEGLEEAIAATKQAELETKQELDAALNELGPDGD 381

RESULT 5
Q9LSB4 PRELIMINARY; PRT; 246 AA.
AC Q9LSB4;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SP198;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=SP198;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253408; AAF67356.1; -.
DR HSP; P05412; 1JNM.
FT NON_TER 246
SQ SEQUENCE 246 AA; 26972 MW; 2190EED1460D26D9 CRC64;

Query Match 23.9%; Score 114.5; DB 2; Length 246;
Best Local Similarity 27.3%; Pred. No. 3;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:32:37 ; Search time 56.9055 Seconds
(without alignments)
863.882 Million cell updates/sec

Title: US-10-674-755-28
Perfect score: 480
Sequence: 1 QALVESTQEIIEELKDYNEQ.....EQDELQAEILDQLLDEVGQE 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 480 | 100.0 | 463 | Q9LAX4 | Q9LAX4 streptococc |
| 2 | 118 | 24.6 | 479 | Q9LAX2 | Q9LAX2 streptococc |
| 3 | 118 | 24.6 | 481 | Q9LAX5 | Q9LAX5 streptococc |
| 4 | 115 | 24.0 | 653 | Q34097 | Q34097 streptococc |
| 5 | 114.5 | 23.9 | 246 | Q915B4 | Q915B4 streptococc |
| 6 | 114.5 | 23.9 | 426 | Q9LAX5 | Q9LAX5 streptococc |
| 7 | 114 | 23.8 | 107 | Q8KQK2 | Q8KQK2 streptococc |
| 8 | 111.5 | 23.2 | 213 | Q8GNS7 | Q8GNS7 streptococc |
| 9 | 111 | 23.1 | 211 | Q8GNT0 | Q8GNT0 streptococc |
| 10 | 111 | 23.1 | 257 | Q91594 | Q91594 streptococc |
| 11 | 110.5 | 23.0 | 224 | Q8GNS8 | Q8GNS8 streptococc |
| 12 | 110.5 | 23.0 | 256 | Q91595 | Q91595 streptococc |
| 13 | 110 | 22.9 | 2301 | Q6BG00 | Q6BG00 paramediu |
| 14 | 109 | 22.7 | 3384 | Q81L42 | Q81L42 plasmodium |
| 15 | 108 | 22.5 | 1024 | Q7R219 | Q7R219 Giardia lam |
| 16 | 107.5 | 22.4 | 227 | Q9KGS0 | Q9KGS0 streptococc |
| 17 | 107.5 | 22.4 | 480 | Q9LAX3 | Q9LAX3 streptococc |
| 18 | 107.5 | 22.4 | 584 | Q96YQ6 | Q96YQ6 sulfolobus |
| 19 | 107 | 22.3 | 395 | Q91AY2 | Q91AY2 streptococc |
| 20 | 107 | 22.3 | 408 | Q9LAY0 | Q9LAY0 streptococc |
| 21 | 107 | 22.3 | 1219 | Q9NJ23 | Q9NJ23 aequipecten |
| 22 | 107 | 22.3 | 1249 | Q9NJ22 | Q9NJ22 aequipecten |
| 23 | 107 | 22.3 | 1243 | Q9NJ21 | Q9NJ21 aequipecten |
| 24 | 107 | 22.3 | 1253 | Q9NJ20 | Q9NJ20 aequipecten |
| 25 | 107 | 22.3 | 1938 | 1 MYS ASQIR | P24773 aequipecten |
| 26 | 107 | 22.3 | 1941 | Q26079 | Q26079 placopecten |
| 27 | 107 | 22.3 | 1950 | Q26080 | Q26080 placopecten |
| 28 | 107 | 22.3 | 1951 | Q17042 | Q17042 aequipecten |
| 29 | 107 | 22.3 | 1979 | 1 TRIA HUMAN | Q15643 homo sapien |
| 30 | 106.5 | 22.2 | 249 | Q9L575 | Q9L575 streptococc |
| 31 | 106 | 22.1 | 1940 | 2 Q9U7E3 | Q9U7E3 pecten maxi |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 32 | 105 | 21.9 | 1162 | 2 | Q98148 | Q98148 human herpe |
| 33 | 104.5 | 21.8 | 461 | 2 | Q9LAX6 | Q9LAX6 streptococc |
| 34 | 104 | 21.7 | 312 | 2 | Q86BL7 | Q86BL7 drosophila |
| 35 | 104 | 21.7 | 566 | 2 | Q9VL65 | Q9VL65 drosophila |
| 36 | 104 | 21.7 | 1945 | 2 | Q9BLD0 | Q9BLD0 patinopecte |
| 37 | 103.5 | 21.6 | 1992 | 2 | Q04834 | Q04834 xenopus lae |
| 38 | 103 | 21.5 | 222 | 2 | Q9L577 | Q9L577 streptococc |
| 39 | 103 | 21.5 | 262 | 2 | Q9L576 | Q9L576 streptococc |
| 40 | 103 | 21.5 | 415 | 2 | Q9LAY7 | Q9LAY7 streptococc |
| 41 | 103 | 21.5 | 739 | 2 | Q9RQT4 | Q9RQT4 streptococc |
| 42 | 103 | 21.5 | 820 | 2 | Q9RQT1 | Q9RQT1 streptococc |
| 43 | 103 | 21.5 | 929 | 2 | Q9KK19 | Q9KK19 streptococc |
| 44 | 103 | 21.5 | 929 | 2 | Q9ZAYS | Q9ZAYS streptococc |
| 45 | 103 | 21.5 | 976 | 2 | Q9DUN0 | Q9DUN0 human herpe |

ALIGNMENTS

| | | | | | |
|-----------------------|--|--|--|--------------|--|
| RESULT 1 | | PRELIMINARY; | | PRT; 463 AA. | |
| Q9LAX4 | | Q9LAX4 | | Q9LAX4 | |
| AC | | Q9LAX4; | | PRT; 463 AA. | |
| DT | | 01-OCT-2000 (TremBLrel. 15, Created) | | | |
| DT | | 01-OCT-2000 (TremBLrel. 15, Last sequence update) | | | |
| DT | | 01-OCT-2003 (TremBLrel. 25, Last annotation update) | | | |
| DE | | PspA (Fragment). | | | |
| GN | | Name=pspA; | | | |
| OS | | Streptococcus pneumoniae. | | | |
| OC | | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | |
| OC | | Streptococcus. | | | |
| OX | | NCBI_TaxID=1313; | | | |
| RN | | [1] | | | |
| RP | | SEQUENCE FROM N.A. | | | |
| RC | | STRAIN-BG6380; | | | |
| RX | | MEDLINE=20448953; PubMed=10992499; | | | |
| RX | | DOI=10.1128/IAI.68.10.5889-5900.2000; | | | |
| RA | | Hollingshead S.K., Becker R., Briles D.E.; | | | |
| RT | | "Diversity of PspA: mosaic genes and evidence for past recombination | | | |
| RT | | in Streptococcus pneumoniae."; | | | |
| RL | | Infect. Immun. 68:5889-5900(2000). | | | |
| DR | | EMBL; AF071823; AAF27717.1; -. | | | |
| FT | | NON_TER 463 | | | |
| SQ | | SEQUENCE 463 AA; 51608 MW; F8663ED2858BBAF CRC64; | | | |
| Query Match | | 100.0%; Score 480; DB 2; Length 463; | | | |
| Best Local Similarity | | 100.0%; Pred. No. 3.1e-24; | | | |
| Matches | | 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | | 1 QALVESTQEIIEELKDYNEQISEGETILILAIQNKISDLDDKIAEAEKKLADSQNGEGVE 60 | | | |
| Db | | 240 QALVESTQEIIEELKDYNEQISEGETILILAIQNKISDLDDKIAEAEKKLADSQNGEGVE 299 | | | |
| QY | | 61 DWYTSGBDDKLEKLAQAEQDELQAEILDQLLDEVGQE 96 | | | |
| Db | | 300 DWYTSGBDDKLEKLAQAEQDELQAEILDQLLDEVGQE 335 | | | |
| RESULT 2 | | PRELIMINARY; | | PRT; 479 AA. | |
| Q9LAX2 | | Q9LAX2 | | Q9LAX2 | |
| ID | | Q9LAX2 | | PRT; 479 AA. | |
| AC | | Q9LAX2; | | | |
| DT | | 01-OCT-2000 (TremBLrel. 15, Created) | | | |
| DT | | 01-OCT-2000 (TremBLrel. 15, Last sequence update) | | | |
| DT | | 01-OCT-2003 (TremBLrel. 25, Last annotation update) | | | |
| DE | | PspA (Fragment). | | | |
| GN | | Name=pspA; | | | |
| OS | | Streptococcus pneumoniae. | | | |
| OC | | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | |
| OC | | Streptococcus. | | | |
| OX | | NCBI_TaxID=1313; | | | |
| RN | | [1] | | | |
| RP | | SEQUENCE FROM N.A. | | | |

Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95013
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <KUR>
A:Cross-references: UNIPROT:Q97T39; GB:AE005672; PIDN:AAK74303.1; PID:gl4971584; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0117

Query Match 20.0%; Score 96; DB 2; Length 744;
Best Local Similarity 30.9%; Pred. No. 15;
Matches 29; Conservative 24; Mismatches 25; Indels 16; Gaps 4;
QY 7 TQEQIEELKDYNEQISEGETLILAIQNKISDLDDKIAEAKKL--ADSQNGEGVEDYWT 64
DB 366 TQDELDKAEAEAEALDKKADE-----LQNKVADLEKEISNLEILLGGADSEDD-----T 413
QY 65 SGDEDKLEKLOAEODELOAEFLDQLDEV--DGOE 96
DB 414 AALQNKLATKKALEKTKQKELDAALNELGPDGDE 447

Search completed: November 17, 2005, 20:39:57
Job time : 13.5461 secs


```

Qy      63 WTSGDDDKLEKQAQDELQAELDQLLDVDGQE 96
        |::| : : : ||: ::|||
Db      258 EVEGTETEEVGEETEVEEGTEVEGTE 291
                                     .

RESULT 10
F75I03
conserved hypothetical protein PAB0812 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75I03
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: F75I03
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-880 <RAW>
A;Cross-references: UNIPROT:QOUZC8; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5013
A;Experimental source: strain Orsay
C;Genetics:
C;Gene: PAB0812
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match          20.5%; Score 98.5; DB 2; Length 880;
Best Local Similarity 25.7%; Pred. No. 12;
Matches 28; Conservative 30; Mismatches 30; Indels 21; Gaps 4;

Qy      4 YESTQE---QIELKDYNQISEGE--EFLILAIQNK-----ISDLDDKIA 44
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     585 FSVESELNLRIOLEEFHDKYVKAEKKSESLRELKNKLEKEKTELDQAFEMLAADVENIE 644

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```

QY      45 EAKKALVDSNGEGVGVIVLWISGSDATKRLQAQLQDDELTAQLDGLTLEVD 93
          |||   |||   |||   :|||   |||   |||   |||   |||
Db      645 EEKAKLKDLSEKFNEEY--EEKRRLVLKLREVSLSLARLEELKKSVE 691
          |||   |||   |||   |||   |||   |||   |||   |||

RESULT 11
A32183
tropomyosin TPM1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2332; protein YNL079C
C;Species: Saccharomyces cerevisiae
C;date: 08-Sep-1989 #sequence revision 08-Sep-1989 #text_change 09-Jul-2004
C;Accession: A32183; S53899; S63011; S63018; S63928

```

A;Residues: 1-199 <LNU>
 A;Cross-references: UNIPROT:P17536; EMBL:M25501; NID:gl73037; PIDN:AAA35174.1; PID:gl73037
 R;Foehlmann, R.; Philippsen, P.
 submitted to the EMBL Data Library, April 1995
 A;Reference number: S53896
 A;Accession: S53899
 A;Molecule type: DNA
 A;Residues: 1-199 <POE>
 A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
 R;Foehlmann, R.; Philippsen, P.
 submitted to the Protein Sequence Database, April 1996
 A;Reference number: S62997
 A;Accession: S63011

A;Residue: 1-199 <POW>
A;Cross-references: EMBL:Z71355; NID:G1301970; PIDN:CAA95953.1; PID:G1301971; MIPS:YNL07
A;Experimental source: Strain S288C
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63018
A;Accession: S63018

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 20:04:33 ; Search time 12.5461 Seconds
(without alignments)
736.230 Million cell updates/sec

Title: US-10-674-755-28

Perfect score: 480

Sequence: 1 QALVESTQEIHELKDYNEQ.....EQDELQAEQLDLDEVDGQE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 107 | 22.3 | 1938 | 1 A40997 | myosin heavy chain |
| 2 | 103.5 | 21.6 | 1992 | 2 A47297 | myosin heavy chain |
| 3 | 102 | 21.2 | 1961 | 1 A61231 | myosin heavy chain |
| 4 | 102 | 21.2 | 1999 | 1 S21801 | myosin heavy chain |
| 5 | 99.5 | 20.7 | 619 | 2 A97887 | surface protein ps |
| 6 | 99.5 | 20.7 | 619 | 2 A41971 | surface protein ps |
| 7 | 99 | 20.6 | 1976 | 2 A59252 | myosin heavy chain |
| 8 | 98.5 | 20.5 | 166 | 2 S73342 | hypothetical prote |
| 9 | 98.5 | 20.5 | 721 | 2 S29795 | hypothetical prote |
| 10 | 98.5 | 20.5 | 880 | 2 F75103 | conserved hypothet |
| 11 | 97.5 | 20.3 | 199 | 2 A32183 | tropomyosin Tpm1 - |
| 12 | 97 | 20.2 | 630 | 2 S29796 | hypothetical prote |
| 13 | 96.5 | 20.1 | 296 | 2 T38993 | microtubule-associ |
| 14 | 96.5 | 20.1 | 670 | 2 T38445 | microtubule-associ |
| 15 | 96 | 20.0 | 744 | 2 F95013 | pneumococcal surfa |
| 16 | 95.5 | 19.9 | 725 | 2 A47168 | cardiac morphogene |
| 17 | 95.5 | 19.9 | 1156 | 2 E69444 | chromosome segrega |
| 18 | 95.5 | 19.9 | 2331 | 2 T25410 | hypothetical prote |
| 19 | 94.5 | 19.7 | 1938 | 2 A59293 | skeletal myosin he |
| 20 | 93.5 | 19.5 | 527 | 2 S33068 | myosin heavy chain |
| 21 | 93.5 | 19.5 | 876 | 2 A23767 | myosin heavy chain |
| 22 | 93.5 | 19.5 | 1940 | 2 A59287 | myosin heavy chain |
| 23 | 93.5 | 19.5 | 2017 | 1 A36014 | myosin heavy chain |
| 24 | 93.5 | 19.5 | 2057 | 2 S61477 | myosin II heavy ch |
| 25 | 93 | 19.4 | 321 | 2 A49369 | mobilization prote |
| 26 | 93 | 19.4 | 446 | 2 A56733 | nuclear domain 10 |
| 27 | 93 | 19.4 | 1738 | 2 T14867 | interaptin - slime |
| 28 | 92.5 | 19.3 | 2007 | 1 B43402 | myosin heavy chain |
| 29 | 91.5 | 19.1 | 676 | 2 S00084 | myosin heavy chain |

30 91.5 19.1 1837 2 T41023
31 91 19.0 264 2 F71466
32 91 19.0 377 2 C69858
33 91 19.0 501 2 A44643
34 91 19.0 1066 2 A81228
35 91 19.0 1938 1 MKRW1
36 90.5 18.9 161 2 S48396
37 90.5 18.9 1577 2 T19722
38 90.5 18.9 1957 2 T38077
39 90 18.8 1056 2 E96748
40 89.5 18.6 1078 2 T18352
41 89.5 18.6 1203 2 B55094
42 89.5 18.6 1790 2 S67593
43 89 18.5 279 2 D71453
44 88.5 18.4 168 2 S73644
45 88.5 18.4 542 2 D81323

ALIGNMENTS

RESULT 1

A40997 myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)
N:Contains: myosin ATPase (BC 3.6.4.1)
C:Species: Aequipecten irradians
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A40997; S13557
R:Nyitrai, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
A:Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Seq
A:Reference number: A40997; MUID:92011595; PMID:1917970
A:Accession: A40997
A:Molecule type: RNA

A:Residues: 1-1938 <NYI>

A:Cross-references: UNIPROT:P24733; GB:X55714; MID:g5611; PIDN:CAA39247.1; PID:g5612
C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b

F:86-763/Domain: myosin motor domain homology <WMOT>

F:176-183/Region: nucleotide-binding motif A (P-loop)

F:547-586/Region: actin binding #status predicted

F:653-675/Region: actin binding #status predicted

F:836-1938/Domain: coiled coil #status predicted <COI>

F:836-1276/Region: S2

F:1277-1938/Region: light meromyosin

F:182/Binding site: ATP (lys) #status predicted

F:693,703/Active site: Cys #status predicted

Query Match 22.3%; Score 107; DB 1; Length 1938;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 29; Conservative 18; Mismatches 33; Indels 28; Gaps 2;

QY 5 ESTQRIEELKDYNEQISEG-----BETLILAIQKISLDDKIAAE 47

Db 1057 KSTQENVDELVRKLEENVRKAEATSSLSKLEDEQNLSVQLQRKIKELQARIELE 1116

QY 48 KKLADSQNGEGVEDWTSGDEDEKLEKLAQAEQLAEQLDLDEVDG 94

Db 1117 BELEARNARA-----KVEKQRAELRELELGERLDEAGG 1152

RESULT 2

A47297

myosin heavy chain form B, nonmuscle - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A47297; A55441

R:Bhatia-Dey, N.; Adelstein, R.S.; Dawid, I.B.

Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993

A:Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmuscul

A:Reference number: A47297; MUID:93219383; PMID:8464900

A:Accession: A47297

A>Status: preliminary; not compared with conceptual translation

XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR N-PSDB; AAS70488.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36660; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2017 AA;
Query Match 22.3%; Score 107; DB 4; Length 2017;
Best Local Similarity 25.6%; Pred. NO. 1;
Matches 31; Conservative 19; Mismatches 29; Indels 42; Gaps 3;
OY 1 QALVESTQEQIEELKDYNEQISEGETL-----ILAIQ----- 33
DB 313 QKLTISRHRREELSDYERIEELENLQQGGSGVIETDLSKIYEMQKTIQVLQIEKVES 372
OY 34 -NKISDLDDKIAEAELKADLQNGSGVEDYWTSGDEDKLEKLAQDELQAEQLDQLDEV 92
DB 373 TKKMEQLDKYDINKLSSAENDRDI-----LRRQEQINVEKKQIMEEC 418
OY 93 D 93
DB 419 E 419

Db 98 GLEEIATKQAELEKTPKELDAALNELGPDGDE 130

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CC molecule from the Rxl strain of Streptococcus pneumoniae.

XX Sequence 653 AA;

Query Match 24.0%; Score 115; DB 8; Length 653;

Best Local Similarity 29.5%; Pred. No. 0.053;

Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;

QY 7 TQEQIEE---LKDYNEQISEGETLILAIQNKISLDLDDKIAEAEKKLADSQNGEGVEDYW 63

DB 296 TQELDKKAEAEAELEKVE-----ALQNQVAEELEELSKELDNLKDAET--NNVEDYI 346

QY 64 TSGDDKLEKLAQDELQAEQLDQLLDEV--DQGE 96

DB 347 KEGLEAEIATKKAEELEKTKELDAALNELGPDGDE 381

RESULT 9

AD052080

ID AD052080 standard; protein; 653 AA.

XX AC

XX AD052080;

XX DT 12-AUG-2004 (first entry)

XX DE

XX S. pneumoniae strain EF5688 PspA protein.

XX KW

XX Immunogenic composition; vaccine; Th2-type immune response;

XX KW pneumococcal surface protein A; PspA.

XX OS

XX Streptococcus pneumoniae.

XX FH

XX Key Location/Qualifiers

XX Peptide 1..31

XX FT /label= Signal_peptide

XX FT 32..653

XX FT /note= "S. pneumoniae strain EF5688 mature PspA protein"

XX FT 110..384

XX FT /note = PspA alpha-helical domain

XX PN US2004101531-A1.

XX XX

XX 27-MAY-2004.

XX XX

XX 15-APR-2003; 2003US-00414532.

XX XX

XX 16-APR-2002; 2002US-0372710P.

XX XX

XX (CURT/) CURTISS R.

XX PA (KANG/) KANG H Y.

XX XX

XX Curtiss R, Kang HY;

XX XX

XX WPI; 2004-399655/37.

XX DR N-PSDB; AD052067.

XX XX

XX New vaccine comprising a live attenuated strain of pathogenic gram-

XX negative bacteria, useful in eliciting a Th2-type immune response in a

XX PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans

XX or bacteria.

XX XX

XX Example 5; SEQ ID NO 26; 94pp; English.

XX PS

XX The invention relates to immunogenic compositions and vaccines comprising

XX a live attenuated strain of pathogenic gram negative bacteria that

XX secretes an antigen. The vaccine is useful in eliciting a Th2-type immune

XX response in a vertebrate against pathogens, e.g., helminths, fungi,

XX viruses, protozoans or bacteria. The present sequence is Streptococcus

XX pneumoniae strain EF5688 pneumococcal surface protein A (PspA). This

XX sequence is used in the exemplification of the invention.

XX XX

XX Sequence 653 AA;

Query Match

Best Local Similarity 24.0%; Score 115; DB 8; Length 653;

Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;

QY 7 TQEQIEE---LKDYNEQISEGETLILAIQNKISLDLDDKIAEAEKKLADSQNGEGVEDYW 63

DB 296 TQELDKKAEAEAELEKVE-----ALQNQVAEELEELSKELDNLKDAET--NNVEDYI 346

QY 64 TSGDDKLEKLAQDELQAEQLDQLLDEV--DQGE 96

DB 347 KEGLEAEIATKKAEELEKTKELDAALNELGPDGDE 381

RESULT 10

ABU08487

ID ABU08487 standard; protein; 8991 AA.

XX AC

XX ABU08487;

XX DT 24-JUN-2003 (first entry)

XX DE

XX S. pneumoniae pneumococcal surface protein A (PspA) protein.

XX KW

XX Pneumococcal surface protein C; PspC; pneumococcal surface protein A;

XX KW alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;

XX KW antibacterial.

XX OS

XX Streptococcus pneumoniae.

XX FH

XX Key Location/Qualifiers

XX FT Misc-difference 1..8991

XX FT /note= "All Xaa residues within this sequence are

XX FT unknown"

XX XX

XX US6500613-B1.

XX XX

XX 31-DEC-2002.

XX XX

XX 16-SEP-1996; 96US-00714741.

XX XX

XX 15-SEP-1995; 95US-00529055.

XX XX

XX (UYAL-) UNIV ALABAMA.

XX XX

XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

XX PI Hollingshead S, Tart R, Brooks-Walter A;

XX XX

XX WPI; 2003-361534/34.

XX DR

XX Isolated PspC amino acid sequence used as polymerase chain reaction or

XX PT hybridization probe, comprises pneumococcal surface protein having alpha-

XX PT helical, proline rich and repeat regions.

XX XX

XX Disclosure; Col 145-188; 186pp; English.

XX XX

XX The present invention relates to the isolation of Streptococcus

XX pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide

XX CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-

XX CC like protein having alpha-helical, proline rich and repeat regions. The

XX CC PspC and PspA proteins may be used in a vaccine to protect against

XX CC pneumococcal infections. The polynucleotide sequences encoding PspC and

XX CC PspA may be used for the expression of the proteins, and as PCR primers

XX CC or hybridisation probes. The present sequence represents S. pneumoniae

XX CC PspA protein

XX XX

XX Sequence 8991 AA;

Query Match

Best Local Similarity 24.0%; Score 115; DB 6; Length 8991;

Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;

QY 7 TQEQIEE---LKDYNEQISEGETLILAIQNKISLDLDDKIAEAEKKLADSQNGEGVEDYW 63

DB 296 TQELDKKAEAEAELEKVE-----ALQNQVAEELEELSKELDNLKDAET--NNVEDYI 346

XX 12-AUG-2004 (first entry)
XX S. pneumoniae strain EF5688 PspA alpha helical domain.
XX Immunogenic composition; vaccine; Th2-type immune response ;
XX pneumococcal surface protein A; PspA.
XX Streptococcus pneumoniae.
XX OS US2004101531-A1.
XX PN 27-MAY-2004.
XX PD 15-APR-2003; 2003US-00414532.
XX PF 16-APR-2002; 2002US-0372710P.
XX PR (CURT/) CURTISS R.
XX PA (KANG/) KANG H Y.
XX PI Curtiss R, Kang HY;
XX XX WPI; 2004-399655/37.
XX New vaccine comprising a live attenuated strain of pathogenic gram-
PT negative bacteria, useful in eliciting a Th2-type immune response in a
PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
PT or bacteria.
XX Claim 17; SEQ ID NO 1; 94pp; English.
XX The invention relates to immunogenic compositions and vaccines comprising
CC a live attenuated strain of pathogenic gram negative bacteria that
CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
CC response in a vertebrate against pathogens, e.g., helminths, fungi,
CC viruses, protozoans or bacteria. The present sequence is Streptococcus
CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
CC helical domain. This sequence is used in the invention.
XX Sequence 275 AA;
SQ Query Match 24.0%; Score 115; DB 8; Length 275;
Best Local Similarity 29.5%; Pred. No. 0.02;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;
QY 7 TQEQIEE---LKDYNEQISEGETLILAIQNKISLDLDDKIAEAEKKLADSQNGEGVEDYW 63
Db 187 TQDELDKAAEAELNEKVE-----ALQNQVAEELEBELSKLEDNLKDAET-NNVEDYI 237
QY 64 TSGDEDKLEKLAQODELQAEILDQLLDEV--DGQE 96
Db 238 KEGLEATATKKAELEKTQKELDAALNELGPDGE 272
RESULT 5
ADK52496
ID ADK52496 standard; protein; 369 AA.
XX ADK52496;
XX 20-MAY-2004 (first entry)
XX alpha helical region PspA molecule from the Rx1 strain.
XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
XX hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
XX Hodgkin's disease.
XX OS Streptococcus pneumoniae.
XX PN WO2004016231-A2.
XX

PD 26-FEB-2004.
XX 17-FEB-2003; 2003WO-US008199.
XX 15-MAR-2002; 2002US-0365351P.
XX (UABR-) UAB RES FOUND.
XX Briles DE;
XX WPI; 2004-192068/18.
XX Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX Claim 17; SEQ ID NO 2; 4lpp; English.
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rx1 strain of Streptococcus
CC pneumoniae.
XX Sequence 369 AA;
SQ Query Match 24.0%; Score 115; DB 8; Length 369;
Best Local Similarity 29.5%; Pred. No. 0.027;
Matches 28; Conservative 28; Mismatches 25; Indels 14; Gaps 4;
QY 7 TQEQIEE---LKDYNEQISEGETLILAIQNKISLDLDDKIAEAEKKLADSQNGEGVEDYW 63
Db 265 TQDELDKAAEAELNEKVE-----ALQNQVAEELEBELSKLEDNLKDAET-NNVEDYI 315
QY 64 TSGDEDKLEKLAQODELQAEILDQLLDEV--DGQE 96
Db 316 KEGLEATATKKAELEKTQKELDAALNELGPDGE 350
RESULT 6
AAW14592
ID AAW14592 standard; protein; 458 AA.
XX AAW14592;
XX 17-OCT-2003 (revised)
DT 27-OCT-1997 (first entry)
XX Streptococcus pneumoniae PspA surface protein.
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
XX bacteraemia; pneumonia.
XX OS Streptococcus pneumoniae; strain Ef5668.
XX WO9709994-A1.
XX 20-MAR-1997.
XX 16-SEP-1996; 96WO-US014819.
XX 15-SEP-1995; 95US-00529055.
XX (UABR-) UAB RES FOUND.
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 68.2194 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-28

Perfect score: 480

Sequence: 1 QALVSTQEQIEELKDYNEQ.....EQDELQAEIQLDLLEVDQGE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 480 | 100.0 | 96 | 2 | AAW46292 Pneumoc |
| 2 | 115 | 24.0 | 232 | 7 | Abw02624 Ef5668c p |
| 3 | 115 | 24.0 | 233 | 2 | AAW14590 Streptoco |
| 4 | 115 | 24.0 | 275 | 8 | Ado52055 S. pneumo |
| 5 | 115 | 24.0 | 369 | 8 | Adk52496 alpha hel |
| 6 | 115 | 24.0 | 458 | 2 | AAW14592 Streptoco |
| 7 | 115 | 24.0 | 458 | 7 | Abw02626 Ef5668 pn |
| 8 | 115 | 24.0 | 653 | 8 | Adk52495 PspA mole |
| 9 | 115 | 24.0 | 653 | 8 | Ado52080 S. pneumo |
| 10 | 115 | 24.0 | 8991 | 6 | Abu08487 S. pneumo |
| 11 | 109 | 22.7 | 211 | 7 | Abw02621 Bg11703c |
| 12 | 109 | 22.7 | 238 | 2 | AAW14587 Streptoco |
| 13 | 108 | 22.5 | 588 | 6 | Abu08491 Coiled co |
| 14 | 107 | 22.3 | 1979 | 7 | Adb75595 Prostata |
| 15 | 107 | 22.3 | 2017 | 4 | Abg06301 Novel hum |
| 16 | 106 | 22.1 | 212 | 2 | AAW14588 Streptoco |
| 17 | 106 | 22.1 | 212 | 7 | Abw02622 Bg7817c p |
| 18 | 105 | 21.9 | 1162 | 3 | AAy96255 Kaposi's |
| 19 | 105 | 21.9 | 1162 | 3 | AAy58500 HHV8 ORF |
| 20 | 105 | 21.9 | 1162 | 4 | AAb62331 Amino aci |
| 21 | 105 | 21.9 | 1162 | 5 | Abb05621 Kaposi's |
| 22 | 105 | 21.9 | 1162 | 8 | ADj65096 HHV8 late |
| 23 | 104.5 | 21.8 | 1231 | 6 | ABU08490 Fragment |
| 24 | 104 | 21.7 | 557 | 4 | ABb67811 Drosophil |
| 25 | 103 | 21.5 | 550 | 8 | Adk48356 Streptoco |

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|----|-------|------|------|---|--------------------|
| 26 | 103 | 21.5 | 550 | 8 | ADR95223 Novel S. |
| 27 | 103 | 21.5 | 589 | 2 | AAy43392 PspC alph |
| 28 | 103 | 21.5 | 865 | 6 | ABu08489 S. pneumo |
| 29 | 103 | 21.5 | 929 | 2 | AAW14593 Streptoco |
| 30 | 103 | 21.5 | 929 | 2 | AAy43384 S. pneumo |
| 31 | 102.5 | 21.4 | 459 | 8 | ADO15316 S. pneumo |
| 32 | 102.5 | 21.4 | 605 | 6 | ABU08493 Fragment |
| 33 | 102 | 21.2 | 188 | 2 | AAW14580 Streptoco |
| 34 | 102 | 21.2 | 188 | 7 | ABW02613 Rct129c p |
| 35 | 102 | 21.2 | 289 | 2 | AAW62276 Streptoco |
| 36 | 102 | 21.2 | 289 | 2 | AAy41840 Streptoco |
| 37 | 102 | 21.2 | 289 | 2 | AAW87910 Protein s |
| 38 | 102 | 21.2 | 289 | 2 | AAW92458 S. pneumo |
| 39 | 102 | 21.2 | 1126 | 8 | ADS24511 Bacterial |
| 40 | 102 | 21.2 | 1963 | 4 | AAW79838 Human pro |
| 41 | 101 | 21.0 | 1976 | 7 | ADe63514 Rat Prote |
| 42 | 101 | 21.0 | 1976 | 7 | ADe63518 Rat Prote |
| 43 | 100.5 | 20.9 | 206 | 2 | AAW14574 Streptoco |
| 44 | 100.5 | 20.9 | 206 | 7 | ABW02608 Db15c pne |
| 45 | 100.5 | 20.9 | 653 | 2 | AAr27150 PspA frag |

ALIGNMENTS

RESULT 1
AAW46292
ID AAW46292 standard; protein; 96 AA.
XX AC AAW46292;
XX AC AAW46292 (first entry)
DT 29-JUL-1998
DE Pneumococcal surface protein As (PspAs) from clade 6 strain BC6380.
XX Streptococcus pneumoniae; vaccine; pneumococcal surface protein As;
KW infection; protection; PspAs.
KW Streptococcus pneumoniae.
OS Streptococcus pneumoniae.
XX WO9811915-A1.
XX 26-MAR-1998.
XX 22-SEP-1997; 97WO-US016761.
XX 20-SEP-1996; 96US-00710749.
XX (CONN-) CONNAUGHT LAB LTD.
XX Becker RS, Briles DE, Hollingshead S;
XX WPI; 1998-217031/19.
PT New vaccines for protection against pneumococcal infection - comprising
at least 2 pneumococcal surface protein As, each selected from a
different family.
XX Example 3; Fig 8; 57pp; English.
PS This is the sequence of a pneumococcal surface protein As (PspAs) from
strain BC6380, a representative strain of clade 6. This can be used in
the preparation of a vaccine composition comprising at least 2 PspAs,
each of which is selected from a different family. The vaccines can
provide for broad range protection against infection by different
Streptococcus pneumoniae strains
XX Sequence 96 AA;

Query Match 100.0%; Score 480; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3e-36;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-22

Query Match          42.4%; Score 257.5; DB 15; Length 106;
Best Local Similarity 49.2%; Pred.No.8.1e-17;
Matches        60; Conservative    17; Mismatches   26; Indels      19; Gaps       4;

Qy     1 LEDSGIGLEKVLATLDPGGTTPDGLDKKEASE---DSNICALPNOVSDLENQVSSELDREVTV 57
         || : || :|||:|||:|||:: : : |||:: | : :: 
Db     1 LEKAEEALENLSTLPDGKTDELKGAAEALNKVKVEALPNQ-----ELEELS 52
         : || : |||:|||:|||:: : |||:: | : :: 

Qy     58 RLPSDLKDTEGNNVGDDYVKKGLEKALTDEKVGLNNTPKALDTAPKALDTALNELPGDGD 117
         : || : |||:|||:|||:: : |||:: | : :: 
Db     53 KLIEDNLDAE--TNVEDIYIEGLEEAIAIKQAELKET-----PRELDAALNELGP DGE 104
         : || : |||:|||:|||:: : |||:: | : :: 

Qy           118 EE 119
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Db           105 EE 106

RESULT 14
US-10-674-755-26
; Sequence 26, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(108)
; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
US-10-674-755-26

Query Match          38.1%; Score 231.5; DB 15; Length 108;
Best Local Similarity 44.7%; Pred.No.2.5e-14;
Matches        55; Conservative    19; Mismatches   30; Indels      19; Gaps       4;

Qy     1 LEDSGIGLEKVLATLDPGGTTPDGLDKKEASE---DSNICALPNOVSDLENQVSSELDREVTV 57
         || : || :|||:|||:|||:: : |||:: | : :: 
Db     1 LEKAEEALENLSTLPDGKTDELKGAAEALNKVKVEALPNPYXEELSP----- 54
         : || : |||:|||:|||:: : |||:: | : :: 

Qy     58 RLPSS-LKDTTEGNNGVDYVKKGLEKALTDEKVGLNNTPKALDTAPKALDTALNELPGDGD 116
         ||| : ||| :|||:|||:|||:: : |||:: | : :: 
Db     55 --PEDLNKAETNHVEDIYIEGLEEAIAIKQAELLEET-----POEVDAALNDLVPDGG 105
         |||

Qy           117 EEE 119
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Db           106 EEE 108

RESULT 15
US-10-299-636-84
; Sequence 84, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
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[illegible]

[illegible]

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US-10-299-636-58
; Sequence 58, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: UNSURE
; LOCATION: (4)
; OTHER INFORMATION: Xaa at position 4 is unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (16)
; OTHER INFORMATION: Xaa at position 16 is unknown
; US-10-299-636-58

Query Match      100.0%; Score 607; DB 15; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.5e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEDSGLEKVLATLDPGGETPDGLDKAESDSNIGALPNOVSDLENQVSELDREVTRLP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      27 LEDSGLEKVLATLDPGGETPDGLDKAESDSNIGALPNOVSDLENQVSELDREVTRLP 86

Qy      61 SDKDTEGNNVGDYVKGLEKALTDKVGKLNTPKALDTAPKALDTALNELGPDGDEE 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      87 SDKDTEGNNVGDYVKGLEKALTDKVGKLNTPKALDTAPKALDTALNELGPDGDEE 145

RESULT 3
US-10-702-305A-18
; Sequence 18, Application US/10702305A
; Publication No. US20040213803A1
; GENERAL INFORMATION:
; APPLICANT: Michael C. Chen
; APPLICANT: Chuang-Jiun Chio
; APPLICANT: Zhongming Li
; APPLICANT: Dong-Sheng Chen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR
; PREVENTING PNEUMOCOCCAL INFECTION
; FILE REFERENCE: 12844-002001
; CURRENT APPLICATION NUMBER: US/10/702,305A
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/424,497
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence

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US-10-702-305A-18
Query Match      71.2%; Score 432; DB 16; Length 459;
Best Local Similarity 77.4%; Pred. No. 1.3e-32;
Matches 89; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy      1 LEDSGLEKVLATLDPGGETPDGLDKAESDSNIGALPNOVSDLENQVSELDREVTRLP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      345 LEDAELEKVLATLDPEGKTQDELDEKAEADANIEALQNKVADLENKVAELDKVEVTRLQ 404

Qy      61 SDKDTEGNNVGDYVKGLEKALTDKVGKLNTPKALDTAPKALDTALNELGPDG 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      405 SDKDAENNVEDYVKGGLDKALTDKKVGLNNTQKALDTAOKALDTALNELGPDG 459

RESULT 4
US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-10-674-755-25

Query Match      49.2%; Score 298.5; DB 15; Length 108;
Best Local Similarity 55.5%; Pred. No. 1e-20;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

Qy      1 LEDSGLEKVLATLDPGGETPDGLDKAESDSNIGALPNOVSDLENQVSELDREVTRLP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 LEDAELEKVLATLDPEGKTQDELDEKAEAE----AELNEKVEALQNOVALEBELSKLE 56

Qy      61 SDKDTEGNNVGDYVKGLEKALTDKVGKLNTPKALDTAPKALDTALNELGPDGDEE 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      57 DNLKDAETNNVEDYIKGLSEAIATKKALEKT-----QKELDAALNELGPDGDEE 108

RESULT 5
US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 232

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 79.1482 Seconds
(without alignments)
629.082 Million cell updates/sec

Title: US-10-674-755-27
Perfect score: 607
Sequence: 1 LEDSGLGLEKVLATDPGCE.....APKALDTALNELPGDGEDEE 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 607 | 100.0 | 119 | 15 | US-10-674-755-27 |
| 2 | 607 | 100.0 | 215 | 15 | US-10-299-636-58 |
| 3 | 432 | 71.2 | 459 | 16 | US-10-702-305A-18 |
| 4 | 298.5 | 49.2 | 108 | 15 | US-10-674-755-25 |
| 5 | 298.5 | 49.2 | 232 | 15 | US-10-299-636-85 |
| 6 | 298.5 | 49.2 | 275 | 16 | US-10-414-532-1 |
| 7 | 298.5 | 49.2 | 458 | 15 | US-10-299-636-88 |
| 8 | 298.5 | 49.2 | 653 | 16 | US-10-414-532-26 |
| 9 | 287.5 | 47.4 | 108 | 15 | US-10-674-755-24 |
| 10 | 280.5 | 46.2 | 212 | 15 | US-10-299-636-83 |
| 11 | 279.5 | 46.0 | 108 | 15 | US-10-674-755-23 |
| | | | | | Sequence 27, Appl |
| | | | | | Sequence 58, Appl |
| | | | | | Sequence 18, Appl |
| | | | | | Sequence 25, Appl |
| | | | | | Sequence 85, Appl |
| | | | | | Sequence 1, Appl |
| | | | | | Sequence 88, Appl |
| | | | | | Sequence 26, Appl |
| | | | | | Sequence 24, Appl |
| | | | | | Sequence 83, Appl |
| | | | | | Sequence 23, Appl |

| | | | | | | |
|----|-------|------|-----|----|-------------------|-------------------|
| 12 | 279.5 | 46.0 | 211 | 15 | US-10-299-636-82 | Sequence 82, Appl |
| 13 | 257.5 | 42.4 | 106 | 15 | US-10-674-755-22 | Sequence 22, Appl |
| 14 | 231.5 | 38.1 | 108 | 15 | US-10-674-755-26 | Sequence 26, Appl |
| 15 | 228.5 | 37.6 | 185 | 15 | US-10-299-636-84 | Sequence 84, Appl |
| 16 | 200.5 | 33.0 | 233 | 15 | US-10-299-636-67 | Sequence 67, Appl |
| 17 | 199 | 32.8 | 230 | 16 | US-10-414-532-32 | Sequence 32, Appl |
| 18 | 199 | 32.8 | 230 | 16 | US-10-414-532-19 | Sequence 19, Appl |
| 19 | 199 | 32.8 | 290 | 16 | US-10-414-532-65 | Sequence 65, Appl |
| 20 | 199 | 32.8 | 487 | 16 | US-10-414-532-34 | Sequence 34, Appl |
| 21 | 199 | 32.8 | 487 | 16 | US-10-414-532-21 | Sequence 21, Appl |
| 22 | 199 | 32.8 | 524 | 16 | US-10-414-532-28 | Sequence 28, Appl |
| 23 | 196.5 | 32.4 | 213 | 15 | US-10-299-636-62 | Sequence 62, Appl |
| 24 | 193.5 | 31.9 | 104 | 15 | US-10-674-755-20 | Sequence 20, Appl |
| 25 | 192.5 | 31.7 | 104 | 15 | US-10-674-755-21 | Sequence 21, Appl |
| 26 | 190.5 | 31.4 | 197 | 15 | US-10-299-636-59 | Sequence 59, Appl |
| 27 | 190.5 | 31.4 | 744 | 10 | US-09-769-787-184 | Sequence 184, App |
| 28 | 190.5 | 31.4 | 744 | 17 | US-10-472-928-32 | Sequence 32, Appl |
| 29 | 189.5 | 31.2 | 641 | 9 | US-09-765-272-160 | Sequence 160, App |
| 30 | 189.5 | 31.2 | 641 | 20 | US-11-106-649-160 | Sequence 160, App |
| 31 | 177.5 | 29.2 | 102 | 15 | US-10-674-755-18 | Sequence 18, Appl |
| 32 | 149.5 | 24.6 | 80 | 15 | US-10-674-755-19 | Sequence 19, Appl |
| 33 | 119.5 | 19.7 | 336 | 15 | US-10-299-636-103 | Sequence 103, App |
| 34 | 113 | 18.6 | 141 | 14 | US-10-254-995-2 | Sequence 2, Appl |
| 35 | 113 | 18.6 | 204 | 15 | US-10-299-636-66 | Sequence 66, Appl |
| 36 | 113 | 18.6 | 589 | 9 | US-09-748-875-14 | Sequence 14, Appl |
| 37 | 113 | 18.6 | 589 | 10 | US-09-298-523B-14 | Sequence 14, Appl |
| 38 | 113 | 18.6 | 589 | 15 | US-10-299-636-97 | Sequence 97, Appl |
| 39 | 113 | 18.6 | 589 | 18 | US-10-341-201-14 | Sequence 14, Appl |
| 40 | 113 | 18.6 | 643 | 15 | US-10-299-636-95 | Sequence 95, Appl |
| 41 | 113 | 18.6 | 670 | 9 | US-09-748-875-63 | Sequence 63, Appl |
| 42 | 113 | 18.6 | 670 | 10 | US-09-298-523B-63 | Sequence 63, Appl |
| 43 | 113 | 18.6 | 670 | 18 | US-10-341-201-63 | Sequence 63, Appl |
| 44 | 113 | 18.6 | 690 | 9 | US-09-748-875-61 | Sequence 61, Appl |
| 45 | 113 | 18.6 | 690 | 10 | US-09-298-523B-61 | Sequence 61, Appl |

ALIGNMENTS

RESULT 1
US-10-674-755-27
; Sequence 27, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-27

Query Match 100.0%; Score 607; DB 15; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | | | | | | | | | | | |
|----|----|-----|-------|------------|---------|--------|----|--------|----|-------|------|------|----|-----|-----|
| Qy | 1 | LED | SLGLG | LEKVLATDPG | ETPDGLD | KEASDS | NI | GALPNQ | VS | DLENQ | VS | ELDR | VT | RLP | 60 |
| Db | 1 | LED | SLGLG | LEKVLATDPG | ETPDGLD | KEASDS | NI | GALPNQ | VS | DLENQ | VS | ELDR | VT | RLP | 60 |
| Qy | 61 | SDL | KDTEG | NVGDYV | KGGLG | EKALTD | EK | VGLNNT | PK | ALDTA | PNEL | PGD | GE | EE | 119 |
| Db | 61 | SDL | KDTEG | NVGDYV | KGGLG | EKALTD | EK | VGLNNT | PK | ALDTA | PNEL | PGD | GE | EE | 119 |

RESULT 2

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; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 26:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match 46.0%; Score 279.5; DB 2; Length 108;
Best Local Similarity 52.1%; Pred. No. 2,1e-21;
Matches 62; Conservative 16; Mismatches 30; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKSEDSNIGALPNQVSDLENQVSELDREVTRL 60
DB 1 LEKAELENLLSTLDPEGKTQDELDEKAAE----AELNKKVEALPNQVSELEELS 56
QY 61 SDLKDTGNNVGDYKGGLEKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119
DB 57 DNLKDAETNNVEDYIKEGLEEAATKQAELEKT-----PKELDAALNELGPDGDEE 108

RESULT 14
US-09-147-875A-23
; Sequence 23, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-23

Query Match 46.0%; Score 279.5; DB 4; Length 108;
Best Local Similarity 52.1%; Pred. No. 2,1e-21;
Matches 62; Conservative 16; Mismatches 30; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKSEDSNIGALPNQVSDLENQVSELDREVTRL 60
DB 1 LEKAELENLLSTLDPEGKTQDELDEKAAE----AELNKKVEALPNQVSELEELS 56
QY 61 SDLKDTGNNVGDYKGGLEKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119
DB 57 DNLKDAETNNVEDYIKEGLEEAATKQAELEKT-----PKELDAALNELGPDGDEE 108

RESULT 15
US-08-529-055-67
; Sequence 67, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-67

Query Match 46.0%; Score 279.5; DB 4; Length 211;
Best Local Similarity 52.1%; Pred. No. 5,2e-21;
Matches 62; Conservative 16; Mismatches 30; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKSEDSNIGALPNQVSDLENQVSELDREVTRL 60
DB 25 LEKAELENLLSTLDPEGKTQDELDEKAAE----AELNKKVEALPNQVSELEELS 80
QY 61 SDLKDTGNNVGDYKGGLEKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119
DB 81 DNLKDAETNNVEDYIKEGLEEAATKQAELEKT-----PKELDAALNELGPDGDEE 132

Search completed: November 17, 2005, 19:32:24
Job time : 24.0363 secs
```

US-08-710-749-22

```

Query Match      46.7%; Score 283.5; DB 2; Length 108;
Best Local Similarity 52.1%; Pred. No. 8.3e-22;
Matches 62; Conservative 17; Mismatches 23; Indels 11; Gaps 2

1 LEDSGLEKVLATLDPGGTTPDGLDKPASEDSNIGALPNQVSDLENQVSELDREVTLP 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 LEKAGAGLGNLSTLDPGKTKQDELQKAAE-----AELNKKVEALPNQVSELELSKLE 56

61 SLDKDTGNNYGVYKGGLEKALTDKVGLNNTPKALDTPAKLTALNELGPGDDEE 119
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 DNLKDAETNHYVEDYIKGLEEAIATKQAELEKTK-----PKELDAALENELGPGDDEE 108
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 11
US-08-710-749-23
; Sequence 23, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-710-749-23

```

[illegible]

RESULT 12
US-08-529-055-68

```

; Sequence 68, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-529-055-68

Query Match 46.2%; Score 280.5; DB 4; Length 212;
Best Local Similarity 51.3%; Pred. No. 4.1e-21;
Matches 61; Conservative 18; Mismatches 29; Indels 11; Gaps 2;

QY 1 LEPSGLGLEKVLATLPGGSTPDLGKEASEDSNIGALPNQVSDLENQVSELDEVRTRLP 60
Db 28 LEVAGAGLMLSTLDPEGTQDELKEAE----AELNKKVVALPNQVAELSEELSKLE 83
QY 61 SLDKDTGEGNVGVDYKVGLEKALTDEKVGUNNTPKALDTAPKALDTALNELGPDGDEE 119
Db 84 DNLKDAETNHVEDYIKEGLEEAATKQAELEK-----PKELDAALNELGPDGDEE 135

RESULT 13
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York

```

```
Query Match          49.2%; Score 298.5; DB 4; Length 232;
Best Local Similarity 55.5%; Pred. No. 6.6e-23;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

Qy 1 LEDSGLEKVLATLDPGGTDPGLDKSESDSNIGALPNQVSDLENQVSELDREVTLRP 60
Db 51 LEDAELEKVLATLDPGGTQDELDKEAAE-----AELNKKVEALQNOVALEBELSKLE 106
Qy 61 SDLKDTGNNVDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 107 DNLKDAETNNVDYIKEGLEEAIAATKAELEKT-----QKELDAALNELGPDGDEEE 158

RESULT 8
US-08-529-055-73
; Sequence 73, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Brilles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Thereof, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-73

Query Match          49.2%; Score 298.5; DB 4; Length 458;
Best Local Similarity 55.5%; Pred. No. 1.6e-22;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

Qy 1 LEDSGLEKVLATLDPGGTDPGLDKSESDSNIGALPNQVSDLENQVSELDREVTLRP 60
Db 276 LEDAELEKVLATLDPGGTQDELDKEAAE-----AELNKKVEALQNOVALEBELSKLE 331
Qy 61 SDLKDTGNNVDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 332 DNLKDAETNNVDYIKEGLEEAIAATKAELEKT-----QKELDAALNELGPDGDEEE 383
```

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RESULT 9
US-09-147-875A-24
; Sequence 24, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-24

Query Match          47.4%; Score 287.5; DB 4; Length 108;
Best Local Similarity 52.1%; Pred. No. 3.2e-22;
Matches 62; Conservative 18; Mismatches 28; Indels 11; Gaps 2;

Qy 1 LEDSGLEKVLATLDPGGTDPGLDKSESDSNIGALPNQVSDLENQVSELDREVTLRP 60
Db 1 LEKAGAGLENLLSTLDPEGKTQDELDKEAAE-----AELNKKVEALPNQVALEBELSKLE 56
Qy 61 SDLKDTGNNVDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 57 DNLKDAETNNVDYIKEGLEEAIAATKAELEKT-----PKELDAALNELGPDGDEEE 108

RESULT 10
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Brilles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
```

```
Query Match      100.0%; Score 607; DB 4; Length 8991;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
Db 3874 LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 3933

QY 61 SDLKDTGNNVGDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 3934 SDLKDTGNNVGDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 3992

RESULT 5
US-08-710-749-24
; Sequence 24, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-24

Query Match      49.2%; Score 298.5; DB 2; Length 108;
Best Local Similarity 55.5%; Pred. No. 2.4e-23;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
Db 1 LEDAELEKVLATLDPGKTQDELDEKAAE----AELNEKVEALQNQVALEELSLE 56

QY 61 SDLKDTGNNVGDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 57 DNLKDAETNNVEDYIKEGLEEAIAATKAELEKT-----QKELDAALNELGPDGDEEE 108

RESULT 6
US-09-147-875A-25
; Sequence 25, Application US/09147875A
; Patent No. 6638516
```

```
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-25

Query Match      49.2%; Score 298.5; DB 4; Length 108;
Best Local Similarity 55.5%; Pred. No. 2.4e-23;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
Db 1 LEDAELEKVLATLDPGKTQDELDEKAAE----AELNEKVEALQNQVALEELSLE 56

QY 61 SDLKDTGNNVGDYVKGGLKALTDKVGKLNNTPKALDTAPKALDTALNELGPDGDEEE 119
Db 57 DNLKDAETNNVEDYIKEGLEEAIAATKAELEKT-----QKELDAALNELGPDGDEEE 108

RESULT 7
US-08-529-055-70
; Sequence 70, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swatlow, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-70
```


Qy

61 SDLKDTGEGNNVDYVKGGLKALTDKVGGLNTPKALDTPAKALDTALNELPGDDEE 119
|||
|||

Db

61 SDLKDTGEGNNVDYVKGGLKALTDKVGGLNTPKALDTPAKALDTALNELPGDDEE 119
|||
|||

RESULT 2

```

US-09-147-875A-27
/ Sequence 27, Application US/09147875A
/ Patent No. 6638516
/ GENERAL INFORMATION:
/ APPLICANT: BECKER et al.
/ TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
/ FILE REFERENCE: 454312-2471
/ CURRENT APPLICATION NUMBER: US/09/147,875A
/ CURRENT FILING DATE: 1999-05-24
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-147-875A-27

```

| | Query Match | Best Local Similarity | 100.0%; | Score 607; | DB 4; | Length 119; | |
|----|--------------|---|---------|------------|-------|-------------|---------|
| | Matches 119; | Conservative | 0; | Mismatches | 0; | Indels | Gaps 0; |
| Qy | 1 | LEDSGLGLEKVLATLDPGGTPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP | 60 | | | | |
| Db | 1 | LEDSGLGLEKVLATLDPGGTPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP | 60 | | | | |
| Qy | 61 | SDLKDTGNNVGDYVYVGKLEKALTDEKVLGNTPKALDTAPKALDTALNELPGGDSEE | 119 | | | | |
| Db | 61 | SDLKDTGNNVGDYVYVGKLEKALTDEKVLGNTPKALDTAPKALDTALNELPGGDSEE | 119 | | | | |

RESULT 3

US-08-529-055-43
 ? Sequence 43, Application US/08529055
 ? Patent No. 6592876
 ? GENERAL INFORMATION:
 ? APPLICANT: Briles, David E.
 ? APPLICANT: McDaniel, Larry S.
 ? APPLICANT: Swiatlo, Edwin
 ? APPLICANT: Yother, Janet
 ? APPLICANT: Brooks-Walter, Alexis
 ? TITLE OF INVENTION: Pneumococcal Genes, Portions
 ? TITLE OF INVENTION: Thereof, Expression Products
 ? TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
 ? TITLE OF INVENTION: Portions and Products
 ? NUMBER OF SEQUENCES: 73
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Curtis, Morris & Safford, P.C.
 ? STREET: 530 Fifth Avenue
 ? CITY: New York
 ? STATE: NY
 ? COUNTRY: USA
 ? ZIP: 10036
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/529,055
 ? FILING DATE: 15-SEP-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Frommer, William S.
 ? REGISTRATION NUMBER: 25,506
 ? REFERENCE/DOCKET NUMBER: 454312-2400
 ? TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (212) 840-3333
;
; TELEFAX: (212) 840-0712
;
; INFORMATION FOR SEQ ID NO: 43:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 215 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; US-08-529-055-43

```

| | | | | |
|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 100.0%; | Score 607; | DB 4; | Length 215; |
| Best Local Similarity | 100.0%; | Pred. No. 1.2e-54; | | |
| Matches 119; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | LEDSGIGLEKVLATLPGGSTPGDLKKEASEDSNIGALPNQVSDLENQVSELREVT | RLP | 60 |
| Db | 27 | LEDSGIGLEKVLATLPGGSTPGDLKKEASEDSNIGALPNQVSDLENQVSELREVT | RLP | 86 |
| Qy | 61 | SDLKDTGNNVGDYVVRGGLEKALTDEKVLGNNTPKALDTAPKALDTALNELGPDGD | DEE | 119 |
| Db | 87 | SDLKDTGNNVGDYVVRGGLEKALTDEKVLGNNTPKALDTAPKALDTALNELGPDGD | DEE | 145 |

RESULT 4

```

US-08-714-741-32
; Sequence 32, Application US/08/714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, FOR
; THE PRODUCTION OF EXPRESSION PRODUCTS THEREOF
; TITLE OF INVENTION: EXPRESSION PRODUCTS OF THE
; GENES OF PNEUMOCOCCAL GENES, FOR THE PRODUCTION
; OF EXPRESSION PRODUCTS THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESS: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-714-741-32

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 22.9113 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-27
Perfect score: 607
Sequence: 1 LEDSGLGLEKVLATLDPGEE.....APKALDTALNELGPDGDEEE 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 607 | 100.0 | 119 | 2 | US-08-710-749-27 |
| 2 | 607 | 100.0 | 119 | 4 | US-09-147-875A-27 |
| 3 | 607 | 100.0 | 215 | 4 | US-08-529-055-43 |
| 4 | 607 | 100.0 | 8991 | 4 | US-08-714-741-32 |
| 5 | 298.5 | 49.2 | 108 | 2 | US-08-710-749-24 |
| 6 | 298.5 | 49.2 | 108 | 4 | US-09-147-875A-25 |
| 7 | 298.5 | 49.2 | 232 | 4 | US-08-529-055-70 |
| 8 | 298.5 | 49.2 | 458 | 4 | US-08-529-055-73 |
| 9 | 287.5 | 47.4 | 108 | 4 | US-09-147-875A-24 |
| 10 | 283.5 | 46.7 | 108 | 2 | US-08-710-749-22 |
| 11 | 283.5 | 46.7 | 108 | 2 | US-08-710-749-23 |
| 12 | 280.5 | 46.2 | 212 | 4 | US-08-529-055-68 |
| 13 | 279.5 | 46.0 | 108 | 2 | US-08-710-749-26 |
| 14 | 279.5 | 46.0 | 108 | 4 | US-09-147-875A-23 |
| 15 | 279.5 | 46.0 | 211 | 4 | US-08-529-055-67 |
| 16 | 257.5 | 42.4 | 106 | 4 | US-09-147-875A-22 |
| 17 | 231.5 | 38.1 | 108 | 2 | US-08-710-749-25 |
| 18 | 231.5 | 38.1 | 108 | 4 | US-09-147-875A-26 |
| 19 | 228.5 | 37.6 | 185 | 4 | US-08-529-055-69 |
| 20 | 200.5 | 33.0 | 104 | 2 | US-08-710-749-20 |
| 21 | 200.5 | 33.0 | 233 | 4 | US-08-529-055-52 |
| 22 | 196.5 | 32.4 | 213 | 4 | US-08-529-055-47 |
| 23 | 193.5 | 31.9 | 104 | 2 | US-08-710-749-19 |
| 24 | 193.5 | 31.9 | 104 | 4 | US-09-147-875A-20 |
| 25 | 192.5 | 31.7 | 104 | 4 | US-09-147-875A-21 |
| 26 | 190.5 | 31.4 | 197 | 4 | US-08-529-055-44 |
| 27 | 189.5 | 31.2 | 641 | 3 | US-08-961-083-160 |

| | | | | | | |
|----|-------|------|------|---|-------------------|--------------------|
| 28 | 189.5 | 31.2 | 641 | 4 | US-09-536-784-160 | Sequence 160, Appl |
| 29 | 177.5 | 29.2 | 102 | 2 | US-08-710-749-21 | Sequence 21, Appl |
| 30 | 177.5 | 29.2 | 102 | 4 | US-09-147-875A-18 | Sequence 18, Appl |
| 31 | 149.5 | 24.6 | 80 | 2 | US-08-710-749-18 | Sequence 18, Appl |
| 32 | 149.5 | 24.6 | 80 | 4 | US-09-147-875A-19 | Sequence 19, Appl |
| 33 | 114.5 | 18.9 | 1231 | 4 | US-08-714-741-41 | Sequence 41, Appl |
| 34 | 114 | 18.8 | 289 | 1 | US-08-072-070-4 | Sequence 4, Appl |
| 35 | 114 | 18.8 | 289 | 1 | US-08-469-434-4 | Sequence 4, Appl |
| 36 | 114 | 18.8 | 289 | 1 | US-08-214-222-4 | Sequence 4, Appl |
| 37 | 114 | 18.8 | 289 | 2 | US-08-467-852A-5 | Sequence 5, Appl |
| 38 | 114 | 18.8 | 289 | 2 | US-08-468-718-4 | Sequence 4, Appl |
| 39 | 114 | 18.8 | 289 | 2 | US-08-247-491A-5 | Sequence 5, Appl |
| 40 | 113 | 18.6 | 141 | 4 | US-09-286-981B-2 | Sequence 2, Appl |
| 41 | 113 | 18.6 | 204 | 4 | US-08-529-055-51 | Sequence 51, Appl |
| 42 | 113 | 18.6 | 864 | 4 | US-08-714-741-40 | Sequence 40, Appl |
| 43 | 112 | 18.5 | 100 | 4 | US-09-147-875A-12 | Sequence 12, Appl |
| 44 | 112 | 18.5 | 198 | 4 | US-08-529-055-61 | Sequence 61, Appl |
| 45 | 112 | 18.5 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-710-749-27
; Sequence 27, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-27

Query Match 100.0%; Score 607; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.4e-55;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKSEDSNIGALPNQVSDLENQVSELDREVTRLP 60
DB 1 LEDSGLGLEKVLATLDPGGETPDGLDKSEDSNIGALPNQVSDLENQVSELDREVTRLP 60

Db 77 LEKLLDLDPEGKTQDELDKEAAEALDKKVEALQNKVADLEKEISNL----- 124
Qy 65 DTEGNNVG DYKGGLEKALTDEKVLNN---TPKA-LDTAPKALDTALNELGPDGDEEE 119
Db 125 -----EILLGGADS--EDDTAALQNKLATKKAELEKTXELDAALNELGPDGDEEE 173

Search completed: November 17, 2005, 20:37:54
Job time : 70.5391 secs

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| | | |
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| | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | |
| OC | Streptococcus. | |
| OX | [1] | |
| RN | SEQUENCE FROM N.A. | |
| RP | STRAIN=115; | |
| RC | MEDLINE=20472698; PubMed=11015380; | |
| RX | Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.; | |
| RA | "Pneumococcal pspA sequence types of prevalent multiresistant | |
| RT | pneumococcal strains in the United States and of internationally | |
| RV | disseminated clones."; | |
| RL | J. Clin. Microbiol. 38:3663-3669(2000). | |
| RJ | [2] | |
| RK | SEQUENCE FROM N.A. | |
| RD | STRAIN=115; | |
| RE | Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. | |
| RF | EMBL; AF254256; AAF68091.1; -- | |
| RG | NON_TER 1 | |
| RH | FT NON TER 209 209 | |
| RI | SQ SEQUENCE 209 AA; 22628 MW; 06FF588F7C3BD5B7 CRC64; | |
| | Query Match 32.4%; Score 196.5; DB 2; Length 209; | |
| | Best Local Similarity 41.9%; Pred.No.2.3e-07; | |
| | Matches 49; Conservative 19; Mismatches 26; Indels 23; Gaps 5; | |
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| QY | 7 GLEKVATLPDGGTDPGLDKSEDSNIGALPNQVSDLENQVSDELREVTRPLPSDLKD 66 : : : : : : : : | |
| DG | 25 GLEKLDSLDPGKTQDELDKEAE-----AELDKADELNQKVADLEKEISNL----- 73 : : : : : : : | |
| QZ | 67 EGNNVDGYVGKGLEKALTDEKVLGN--TPKA-LDTAPKALDTALNELPGDGDEE 119 : | |
| DJ | 74 -----EILGGADP--EDDTAAQNKLATTCAELETKQEKDAALNALNELPGDGDEE 122 : | |
| | RESULT 15 | |
| QYL562 | ID Q9LS562 PRELIMINARY; PRT; 242 AA. | |
| AC | OCT-2000 (TrEMBLrel. 15, Created) | |
| CD | OCT-2000 (TrEMBLrel. 15, Last sequence update) | |
| DF | OCT-2000 (TrEMBLrel. 15, Last annotation update) | |
| DI | PepA (Fragment). | |
| DN | Name=PSP-A; | |
| DO | Streptococcus pneumoniae. | |
| DR | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | |
| DU | Streptococcus. | |
| DV | [1] | |
| DW | NCBI_TaxID=1313; | |
| DX | SEQUENCE FROM N.A. | |
| DY | STRAIN=69; | |
| DZ | MEDLINE=20472698; PubMed=11015380; | |
| EI | Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.; | |
| EJ | "Pneumococcal pspA sequence types of prevalent multiresistant | |
| EK | pneumococcal strains in the United States and of internationally | |
| EL | disseminated clones."; | |
| EN | J. Clin. Microbiol. 38:3663-3669(2000). | |
| EO | [2] | |
| EP | SEQUENCE FROM N.A. | |
| EQ | STRAIN=69; | |
| ER | Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. | |
| ES | EMBL; AF255908; AAF70098.1; -- | |
| ET | NON_TER 1 | |
| EU | FT NON TER 242 242 | |
| EV | SQ SEQUENCE 242 AA; 25843 MW; 707EA930797D2C82 CRC64; | |
| | Query Match 32.4%; Score 196.5; DB 2; Length 242; | |
| | Best Local Similarity 42.9%; Pred.No.2.8e-07; | |
| | Matches 51; Conservative 14; Mismatches 25; Indels 29; Gaps 5; | |
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| QY | 8 LEKVATLPDGGTDPGLDKSEASNDSTNGALPNQVSDLENQVSDELREVTRPLPSDLK 64 : : : : : : : | |

[illegible]

| | | | |
|---|--|--|-----|
| Qy | 1 | LEDSGLGLEKVLATLDPGGETDGLDKAESDSNIGALPNQVSDLENQVSELDREVTRLP | 6 |
| Dd | 1 | LKAERAEENLLSTLDPEGKTODELDKEAAE-----AELNKVKYEAQNQVAELEESLSKUE | 56 |
| Qy | 61 | SOLDKTEGNNGVDYKGGLEGKALTDEKVGNNTPKALDTAPKALDTALNELGPDCGDEE | 118 |
| Dd | 57 | DNLKDAETNNVEDYIKEGLEEAIATKKAELEKT-----QKELDAALNELGPGCGDEE | 107 |
| RESULT 11 | | | |
| ID | Q8GNS7 | PRELIMINARY; PRT; 213 AA. | |
| AC | Q8GNS7; | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Created) | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | PepA (Fragment). | | |
| DN | Name=pspA; | | |
| OS | Streptococcus pneumoniae. | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | |
| OC | Streptococcus. | | |
| OX | NCBI_TaxID=1313; | | |
| [1] | | | |
| RN | SEQUENCE FROM N.A. | | |
| RP | STRAIN=128; | | |
| RC | MEDLINE=22241996; PubMed=12354862; | | |
| RA | Dicuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A., | | |
| RX | Lorino G., Recchia S., Pantosti A., Beall B.; | | |
| RT | "Genotypes of invasive pneumococcal isolates recently recovered from | | |
| RT | Italian patients."; | | |
| RL | J. Clin. Microbiol. 40:3660-3665(2002). | | |
| DR | EMBL; AF490268; AAN37736.1; -. | | |
| FT | NON_TER 1 | | |
| FT | NON_TER 213 213 | | |
| SQ | SEQUENCE 213 AA; 23430 MW; 23B4428409526EAB CRC64; | | |
| Query Match 43.6%; Score 264.5; DB 2; Length 213; Best Local Similarity 49.6%; Pred. No. 1.6e-12; Matches 59; Conservative 19; Mismatches 30; Indels 11; Gaps | | | |
| Qy | 1 | LEDSGLGLEKVLATLDPGGETDGLDKAESDSNIGALPNQVSDLENQVSELDREVTRLP | 60 |
| Dd | 26 | LKAERAEENLLSTLDPEGKTODELDKETAE----AELNKVKYEAQNQVAELEESLSKUE | 81 |
| Qy | 61 | SOLDKTEGNNGVDYKGGLEGKALTDEKVGNNTPKALDTAPKALDTALNELGPDCGDEE | 119 |
| Dd | 82 | DNLKVAETNNVEDYIKEGLEEAIATKKAELEKT-----QKALDTALNELGPGCGDEE | 133 |
| RESULT 12 | | | |
| ID | Q9LAX3 | PRELIMINARY; PRT; 480 AA. | |
| AC | Q9LAX3; | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | | |
| DE | PepA (Fragment). | | |
| DN | Name=pspA; | | |
| OS | Streptococcus pneumoniae. | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | |
| OC | Streptococcus. | | |
| OX | NCBI_TaxID=1313; | | |
| [1] | | | |
| RN | SEQUENCE FROM N.A. | | |
| RP | STRAIN=BG7561; | | |
| RC | MEDLINE=20448953; PubMed=10992499; | | |
| RA | DOI=10.1128/JAI.68.10.5889-5900.2000; | | |
| RX | Hollingshead S.K., Becker R., Briles D.E.; | | |
| RT | "Diversity of pSpA: mosaic genes and evidence for past recombination | | |
| RT | in Streptococcus pneumoniae"; | | |
| RL | Infect. Immun. 68:5889-5900(2000). | | |
| DR | EMBL; AF071824; AAF27718.1; -. | | |
| DR | InterPro; IPR005533; Tropomyosin. | | |

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Query Match          70.8%; Score 430; DB 2; Length 211;
Best Local Similarity 74.8%; Pred. No. 3.7e-25;
Matches 89; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
DB 5 LEKAEAELENLLSTLDPEGKTQDELDEKAAE-----AELNKVQALQNVAALEELSKLE 64

QY 61 SLDKDTGNNVGDYVKGGLKALTDKVGNNTPKALDTAPKALDTALNELGPDGDEEE 119
DB 65 SLDKDAENNVEDYVKGGLKALTDKVGNNTPKALDTAPKALDTALNELGPDGDEEE 123

RESULT 6
O34097 PRELIMINARY; PRT; 653 AA.
AC O34097;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PspA.
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF5668;
RX MEDLINE=98427139; PubMed=9746574;
RA McDaniel L.S., McDaniel D.O., Hollingshead S.K., Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
RT to the previously identified PspA sequence from strain Rxl and ability
RT of PspA from EF5668 to elicit protection against pneumococci of
RT different capsular types.";
RL Infect. Immun. 66:4748-4754 (1998) .
DR EMBL; U89711; AAC62252.1; -.
DR HSP; P06653; IHXC.
DR InterPro; IPR002479; CW binding.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR009053; Pfefoldin.
DR Pfam; PF01473; CW binding_1; 9.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
DR SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

Query Match          49.2%; Score 298.5; DB 2; Length 653;
Best Local Similarity 55.5%; Pred. No. 1.5e-14;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
DB 276 LEKAELEKVLATLDPGGTQDELDEKAAE-----AELNKVQALQNVAALEELSKLE 331

QY 61 SLDKDTGNNVGDYVKGGLKALTDKVGNNTPKALDTAPKALDTALNELGPDGDEEE 119
DB 332 DNLKDAETNNVEDYIKEGLEEAATKAELEKT-----QKELDAALNELGPDGDEEE 383

RESULT 7
Q9LSB4 PRELIMINARY; PRT; 246 AA.
AC Q9LSB4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]

Query Match          44.7%; Score 271.5; DB 2; Length 479;
Best Local Similarity 50.4%; Pred. No. 1.2e-12;
Matches 60; Conservative 18; Mismatches 30; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
DB 295 LEKAEAELENLLSTLDPEGKTQDELDEKAAE-----AELNKVQALQNVAALEELSKLE 350

QY 61 SLDKDTGNNVGDYVKGGLKALTDKVGNNTPKALDTAPKALDTALNELGPDGDEEE 119
DB 351 DNLKDAETNNVEDYIKEGLEEAATKAELEKT-----QKELDAALNELGPDGDEEE 402
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RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254254; AAF68089.1; -.
FT NON_TER 1
FT NON_TER 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match 75.1%; Score 456; DB 2; Length 256;
Best Local Similarity 79.0%; Pred. No. 4.8e-27;
Matches 94; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 LEDSGLGLEKVLATDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 LEDAELEKVLATDPGKTDQLDKEAEDANIEALQNKVADLENKVSELDREVTRLQ 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SDLKDTGNNVDYVKGLEKALTDEKVLNNTPKALDTPAKALDTALNELGPDGDEE 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 SDLKDAEENNVEDYVKGLEKALTDEKVLNNTQKALDTAOKALDTALNELGPDGDEE 170
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RESULT 3
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ID Q9KGS0 PRELIMINARY; PRT; 227 AA.
AC Q9KGS0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE PspA protein (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RA Beall B.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288751; AAF91495.1; -.
FT NON_TER 1
FT NON_TER 227
SQ SEQUENCE 227 AA; 24994 MW; 9D24C706228052A6 CRC64;

Query Match 74.6%; Score 453; DB 2; Length 227;
Best Local Similarity 78.2%; Pred. No. 7e-27;
Matches 93; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 LEDSGLGLEKVLATDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LEDAELEKVLATDPGKTDQLDKEAEDANIEALQNKVADLENKVSELDREVTRLQ 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SDLKDTGNNVDYVKGLEKALTDEKVLNNTPKALDTPAKALDTALNELGPDGDEE 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 SDLKDAEENNVEDYVKGLEKALTDEKVLNNTQKALDTAOKALDTALNELGPDGDEE 141
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RESULT 4
Q9L594
ID Q9L594 PRELIMINARY; PRT; 257 AA.
AC Q9L594;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254255; AAF68090.1; -.
FT NON_TER 1
FT NON_TER 257
SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 71.3%; Score 433; DB 2; Length 257;
Best Local Similarity 74.8%; Pred. No. 2.7e-25;
Matches 89; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LEDSGLGLEKVLATDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 51 LEKAELEENLLSTLDPEGKTDQLDKEAEDANIEALQNKVADLENKVSELDREVTRLQ 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SDLKDTGNNVDYVKGLEKALTDEKVLNNTPKALDTPAKALDTALNELGPDGDEE 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 SDLKDAEENNVEDYVKGLEKALTDEKVLNNTQKALDTAOKALDTALNELGPDGDEE 169
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q8GNT0
ID Q8GNT0 PRELIMINARY; PRT; 211 AA.
AC Q8GNT0;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP95;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490265; AAN37733.1; -.
FT NON_TER 1
FT NON_TER 211
SQ SEQUENCE 211 AA; 23207 MW; 096BFBE0B8CD6483 CRC64;
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:32:37 ; Search time 70.5391 Seconds
(without alignments)
863.882 Million cell updates/sec

Title: US-10-674-755-27
Perfect score: 607
Sequence: 1 LEDSGLGLEKVLATLDPGGE.....APKALDTALNELGPDGDEEE 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 464 | 76.4 | 461 | 2 Q9LAX6 | Q9LAX6 streptococc |
| 2 | 456 | 75.1 | 256 | 2 Q9L595 | Q9L595 streptococc |
| 3 | 453 | 74.6 | 227 | 2 Q9KGS0 | Q9KGS0 streptococc |
| 4 | 433 | 71.3 | 257 | 2 Q9L594 | Q9L594 streptococc |
| 5 | 430 | 70.8 | 211 | 2 Q8GNT0 | Q8GNT0 streptococc |
| 6 | 298.5 | 49.2 | 653 | 2 Q34097 | Q34097 streptococc |
| 7 | 275.5 | 45.4 | 246 | 2 Q9L5B4 | Q9L5B4 streptococc |
| 8 | 271.5 | 44.7 | 479 | 2 Q9LAX2 | Q9LAX2 streptococc |
| 9 | 271.5 | 44.7 | 481 | 2 Q9LAX5 | Q9LAX5 streptococc |
| 10 | 270.5 | 44.6 | 107 | 2 Q8KQK2 | Q8KQK2 streptococc |
| 11 | 264.5 | 43.6 | 213 | 2 Q8GNS7 | Q8GNS7 streptococc |
| 12 | 248.5 | 40.9 | 480 | 2 Q9LAX3 | Q9LAX3 streptococc |
| 13 | 197.5 | 32.5 | 222 | 2 Q9L584 | Q9L584 streptococc |
| 14 | 196.5 | 32.4 | 209 | 2 Q9L593 | Q9L593 streptococc |
| 15 | 196.5 | 32.4 | 242 | 2 Q9L562 | Q9L562 streptococc |
| 16 | 190.5 | 31.4 | 228 | 2 Q9L5B8 | Q9L5B8 streptococc |
| 17 | 190.5 | 31.4 | 235 | 2 Q9L582 | Q9L582 streptococc |
| 18 | 190.5 | 31.4 | 249 | 2 Q9L585 | Q9L585 streptococc |
| 19 | 190.5 | 31.4 | 249 | 2 Q9L5D4 | Q9L5D4 streptococc |
| 20 | 190.5 | 31.4 | 252 | 2 Q9L583 | Q9L583 streptococc |
| 21 | 190.5 | 31.4 | 256 | 2 Q9L590 | Q9L590 streptococc |
| 22 | 190.5 | 31.4 | 360 | 2 Q8KQK3 | Q8KQK3 streptococc |
| 23 | 190.5 | 31.4 | 429 | 2 Q9LAX7 | Q9LAX7 streptococc |
| 24 | 190.5 | 31.4 | 526 | 2 Q9LAX9 | Q9LAX9 streptococc |
| 25 | 190.5 | 31.4 | 608 | 2 Q8VQ55 | Q8VQ55 streptococc |
| 26 | 190.5 | 31.4 | 744 | 2 Q97T39 | Q97T39 streptococc |
| 27 | 189.5 | 31.2 | 231 | 2 Q9L579 | Q9L579 streptococc |
| 28 | 189.5 | 31.2 | 241 | 2 Q9L580 | Q9L580 streptococc |
| 29 | 189.5 | 31.2 | 249 | 2 Q9L5B7 | Q9L5B7 streptococc |
| 30 | 185.5 | 30.6 | 502 | 2 Q9LAX8 | Q9LAX8 streptococc |
| 31 | 113 | 18.6 | 417 | 2 Q9LAY3 | Q9LAY3 streptococc |

| | | | | | |
|----|-----|------|-----|----------|--------------------|
| 32 | 113 | 18.6 | 739 | 2 Q9RQT4 | Q9RQT4 streptococc |
| 33 | 113 | 18.6 | 820 | 2 Q9RQT1 | Q9RQT1 streptococc |
| 34 | 113 | 18.6 | 929 | 2 Q9KKI9 | Q9KKI9 streptococc |
| 35 | 113 | 18.6 | 929 | 2 Q9ZAY5 | Q9ZAY5 streptococc |
| 36 | 112 | 18.5 | 619 | 2 Q54972 | Q54972 streptococc |
| 37 | 112 | 18.5 | 619 | 2 Q8DRI0 | Q8DRI0 streptococc |
| 38 | 108 | 17.8 | 415 | 2 Q9LAY1 | Q9LAY1 streptococc |
| 39 | 107 | 17.6 | 99 | 2 Q8KQK4 | Q8KQK4 streptococc |
| 40 | 106 | 17.5 | 224 | 2 Q8GNS8 | Q8GNS8 streptococc |
| 41 | 106 | 17.5 | 249 | 2 Q9L575 | Q9L575 streptococc |
| 42 | 106 | 17.5 | 395 | 2 Q9LAY2 | Q9LAY2 streptococc |
| 43 | 106 | 17.5 | 408 | 2 Q9LAY0 | Q9LAY0 streptococc |
| 44 | 106 | 17.5 | 426 | 2 Q9LAY5 | Q9LAY5 streptococc |
| 45 | 106 | 17.5 | 437 | 2 Q9LAY4 | Q9LAY4 streptococc |

ALIGNMENTS

RESULT 1

| | | | |
|-----------------------|--|--------------------|----------------------------------|
| Q9LAX6 | PRELIMINARY; | PRT; | 461 AA. |
| AC | Q9LAX6; | | |
| DT | 01-OCT-2000 (TremBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TremBLrel. 15, Last sequence update) | | |
| DT | 01-MAR-2003 (TremBLrel. 23, Last annotation update) | | |
| DE | PspA (Fragment). | | |
| GN | Name=pspA; | | |
| OS | Streptococcus pneumoniae. | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | |
| OC | Streptococcus. | | |
| OX | NCBI_TaxID=1313; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=ATCC6303; | | |
| RX | MEDLINE=20448953; PubMed=10992499; | | |
| RX | DOI=10.1128/IAI.68.10.5889-5900.2000; | | |
| RA | Hollingshead S.K., Becker R., Briles D.E.; | | |
| RT | "Diversity of PspA: mosaic genes and evidence for past recombination | | |
| RT | in Streptococcus pneumoniae"; | | |
| RL | Infect. Immun. 68:5889-5900(2000). | | |
| DR | EMBL; AF071820; AAF27715.1; -. | | |
| FT | NON_TER 461 461 | | |
| SQ | SEQUENCE 461 AA; 51563 MW; 249435F65585BB92 CRC64; | | |
| Query Match | 76.4%; | Score 464; | DB 2; Length 461; |
| Best Local Similarity | 79.8%; | Pred. No. 2.3e-27; | |
| Matches | 95; | Conservative 10; | Mismatches 14; Indels 0; Gaps 0; |

| | | | |
|----|---|--|--|
| QY | 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60 | | |
| Db | 273 LEDAELEKVLATLDPEGKTQDELDKEAEDANIEALQNKVADLENKVAEIDKEVTRLQ 332 | | |
| QY | 61 SLDKDTGNNVGVYKGLGKALTDKGLNNTPKALDTAPKALDTALNELGPDGDEEE 119 | | |
| Db | 333 SLDKDAEENNVEDYKGLGKALTDKKVELNNTQKALDTAPKALDTALNELGPDGDEEE 391 | | |

RESULT 2

| | | | |
|--------|--|------|---------|
| Q9L595 | PRELIMINARY; | PRT; | 256 AA. |
| ID | Q9L595 | | |
| AC | Q9L595; | | |
| DT | 01-OCT-2000 (TremBLrel. 15, Created) | | |
| DT | 01-OCT-2000 (TremBLrel. 15, Last sequence update) | | |
| DT | 01-OCT-2003 (TremBLrel. 25, Last annotation update) | | |
| DE | PspA (Fragment). | | |
| GN | Name=pspA; | | |
| OS | Streptococcus pneumoniae. | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | |
| OC | Streptococcus. | | |
| OX | NCBI_TaxID=1313; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |

Db 1043 LEDSLEREKRAPADLDKOKRKEGELKIAQE--NIDESGRORHDLNNLKKKESLHSHVS 1100
Qy 61 SDLKDTGEG--NNVGDYVKGG-----LEKALTDEKVGVLNNTFPKALDTAPKALDTALNEIG 112
Db 1101 SRLEDEQALVSKLQRQIKDQGSRISELEEELENER---QSRSKA-DRAKSDIQRELEELG 1156
Qy 113 PDGDEE 118
Db 1157 EKLDEQ 1162

Search completed: November 17, 2005, 20:39:56
Job time : 17.5519 secs

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Qy      92 NTPKALDTAPKALDITAINELGPDGD 116
          |   ||| :||| :|||
          ||::|||:|||:|
Db     191 TTKATLESAKTALDAVAAKRPDLD 215

RESULT 15
MWKW
myosin heavy chain B [similarity] - Caenorhabditis elegans
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Caenorhabditis elegans
C:date: 13-Jun-1983 #sequence revision 19-May-2000 #text change 09-Jul-2004
C:Accession: TD0770; T21629; A93958; A93287; A21074; A02992
R:Kershaw, J.
```

A;Accession: 121823
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1963 <W12>
A;Cross-references: EMBL:Z83107; PIDN:CAB05505.1; GSPDB:GN00019; CESP:Fl1C3.3
A;Experimental source: clone F32A7
P;Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy c
A;Reference number: A93958; MUID:83273600; PMID:6576334
A;Accession: A93958
A;Molecule type: DNA
A;Residues: 1-61, 'EMSVO', 65-376, 'V', 378-1963 <KAR>
A;Cross-references: GB:J01050; NID:g156399; PIDN:AAA28124.1; PID:g156400
R;McLachlan, A.D.; Karn, J.
Nature 299, 226-231, 1982
A;Title: Periodic charge distributions in the myosin rod amino acid sequence match cross
A;Reference number: A93287; MUID:82272395; PMID:7202124

A;Accession: A93287; PMID:7202124
A;Reference number: A93287; PMID:82272359;
A;Accession: A93287
A;Molecule type: DNA
A;Residues: 847-1333; 'R',1335-1876,'L',1878-1963 <MCL>
A;R;Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H.
Cell 33, 575-583 1983
A;Title: The genes sup-7 X and sup-5 III of *Caenorhabditis elegans* suppress amber nonsense mutations
A;Reference number: A21074; PMID:83232892; PMID:65716395
A;Accession: A21074
A;Molecule type: DNA
A;Residues: 1873-1963 <WI>
A;Cross-references: GB:V01494; GB:J01049; NID:96783; PIDN:CAA24738.1; PID:96784
C;Genetics:
A;Gene: unc-54; CESP:F11C3.3
A;Map position: 1
A;Insertions: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle C
F;84-775/Domain: myosin motor domain homology <MMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;662-684/Region: actin binding #status predicted
F;766-780/Region: actin binding #status predicted
F;848-1963/Domain: coiled coil #status predicted <COI>
F;848-1162/Region: S2
F;1163-1963/Region: light meromyosin
F;125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;702-712/Active site: Cys #status predicted

```

F;848-1163/Domain: collared coil #status predicted <coll>
F;848-1162/Region: S2
F;1163-1963/Region: light meromyosin
F;125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;702,712/Active site: Cys #status predicted

Query Match          13.8%; Score 84; DB 1; Length 1963;
Best Local Similarity 31.0%; Pred. No. 1.2e+02;
Matches 39; Conservative 18; Mismatches 55; Indels 14; Gaps 5;

Qy 1 LEDSGLGLEKVLATDPFGGTPDGLGKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
      ||||| : : : : : |||||

```

A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics: 14.3%; Score 86.5; DB 2; Length 432;
A:Gene: musfiblp
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>
Query Match 14.3%; Score 86.5; DB 2; Length 432;
Best Local Similarity 30.0%; Pred. No. 12;
Matches 30; Conservative 13; Mismatches 34; Indels 23; Gaps 4;
Qy 16 DPGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLPSDLKOTEGNNGVDYV 75
Db 106 DPGGNGNG--AETAEDS-----RQVELESQVKNLSSELK-----NAKDOI 144
Qy 76 KGSLEKALTDEKVGNNTPKALDTAPKALDTALNELGPDG 115
Db 145 QGLQRLTTLHLVNNNIENYVDNKVANLTVVNSL--DG 182
RESULT 10
A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:87175527; PMID:3550794
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <KOY>
A:Cross-references: UNIPROT:P12804; GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387150
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>
Query Match 14.3%; Score 86.5; DB 2; Length 432;
Best Local Similarity 30.0%; Pred. No. 12;
Matches 30; Conservative 13; Mismatches 34; Indels 23; Gaps 4;
Qy 16 DPGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLPSDLKOTEGNNGVDYV 75
Db 106 DPGGNGNG--AETAEDS-----RQVELESQVKNLSSELK-----NAKDOI 144
Qy 76 KGSLEKALTDEKVGNNTPKALDTAPKALDTALNELGPDG 115
Db 145 QGLQRLTTLHLVNNNIENYVDNKVANLTVVNSL--DG 182
RESULT 11
H71977
hypothetical protein jhp0074 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: H71977
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho-
A:Reference number: A71800; MUID:95120557; PMID:9923682
A:Accession: H71977
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <ARN>
A:Cross-references: UNIPROT:Q92MY8; GB:AE001446; GB:AE001439; NID:g4154573; PIDN:AA005646
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0074
Query Match 14.3%; Score 86.5; DB 2; Length 590;
Best Local Similarity 24.4%; Pred. No. 18;
Matches 32; Conservative 26; Mismatches 48; Indels 25; Gaps 5;

| | | | | | |
|----|-----|---|----------------|------------|------|
| Qy | 15 | LDPGGETPGLD-KEASES--- | NIGALPNOV----- | SDLEN----- | Q 48 |
| Db | 385 | LNAGAITDIDIREWTOOSLENNIGIVQODVFLFGGSIRENTAYGKLNASDDEIMVAAQ | | | 4444 |
| Qy | 49 | VSELDREVTRLPSDLKOTEGNNVGVYKGLEKALTDEKVGLENNTP-KALDTAPKALDTA | | | 107 |
| Db | 445 | RARLDELITSSLEGL-DTLVGERGVKLSGGQKQRLSIARFLKNNPPIILDEATSALDTA | | | 503 |
| Qy | 108 | LNE 110 | | | |
| Db | 504 | TEO 506 | | | |

RESULT 8

RESULT 8
JN0666
dnaK-type molecular chaperone hsc3 precursor - fruit fly (*Drosophila melanogaster*)
N/Alternate names: heat-shock cognate protein 3
C/Species: *Drosophila melanogaster*
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0666
R/Rubin, D.M.; Mehta, A.D.; Zhu, J.; Shoham, S.; Chen, X.; Wells, Q.R.; Palter, K.B.
Gene 128, 155-163, 1993
A/Title: Genomic structure and sequence analysis of *Drosophila melanogaster* HSC70 genes
A/Reference number: JN0666; MUID:33292982; PMID:8514184
A/Accession: JN0666
A/Molecule type: DNA
A/Residues: 1-656 <RUB>
A/Cross-references: UNIPROT:Q9YUJ3; GB:L01498
C/Comment: This protein is a member of the heat-shock cognate proteins that are implicated in endocytotic vesicles.

C;Genetics:
A;Gene: hsc3
A;Cross-references: FlyBase:FBgn0001218
A;Introns: 42/2
C;Function:
A;Description: involved in protein folding and assembling/disassembling of pro
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-656/Product: heat-shock cognate protein 3 #status predicted <WAT>

Query Match 14.8%; Score 90; DB 2; Length 656;
Best Local Similarity 30.2%; Pred. No. 11;
Matches 38; Conservative 12; Mismatches 44; Indels 32; Gaps 6

AF0211

```

QY      54  REVTRLPSDLKDTGTENNVGDVVKGLEKALTDKVKGLNNTPKALDTPAKALDTAALNELGP 113
          :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      574  -----NQIGDKDXKLGG-AKLSDDEXTKLSE-----AIDESIKWL-----EQNP 609
          :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |

QY      114  DGDEEE 119
          ||| |
Db      610  DADPEE 615
          ||| |

RESULT 9
I56934
fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:title: Association of mouse fibrinogen-like protein with murine hepatitis virus
A:Reference number: I56934; MUID:95333285; PMID:7609073
A:Accession: I56934
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
```

RESULTS 4
A26655
myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)

A;genome: prasmid pm11

| | | | | |
|-----------------------|-------|---------------|-------|--------------|
| Query Match | 15.7% | Score 95; | DB 2; | Length 1492; |
| Best Local Similarity | 26.3% | Pred. NO. 11; | | |

| | | | | |
|-----------------------|--------|---------------|-------|----------------|
| Query Match | 15.7%; | Score 95; | DB 2; | Length 1492; |
| Best Local Similarity | 26.3%; | Pred. No. 11; | | |
| Matches | 36; | Conservative | 27; | Mismatches 40; |
| | | | | Indels 34; |
| | | | | Gaps 5; |

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|--------|-----------------------|
| | Score | Match | Length | | | |
| 1 | 190.5 | 31.4 | 744 | 2 | F95013 | pneumococcal surfa |
| 2 | 112 | 18.5 | 619 | 2 | A97887 | surface protein ps |
| 3 | 112 | 18.5 | 619 | 2 | A41971 | surface protein ps |
| 4 | 103.5 | 17.1 | 2116 | 2 | A26655 | myosin heavy chain |
| 5 | 95 | 15.7 | 1492 | 2 | T14652 | protein J - Yersin |
| 6 | 95 | 15.7 | 1545 | 2 | T14966 | phage lambda-relat |
| 7 | 91 | 15.0 | 572 | 2 | AF0211 | probable ABC trans |
| 8 | 90 | 14.8 | 656 | 2 | JN0666 | dnak-type molecula |
| 9 | 86.5 | 14.3 | 432 | 2 | I56934 | fibrogen-like pr |
| 10 | 86.5 | 14.3 | 432 | 2 | I27447 | cytotoxic T-lympho |
| 11 | 86.5 | 14.3 | 590 | 2 | H71977 | hypothetical prote |
| 12 | 85.5 | 14.1 | 2022 | 2 | T43214 | ovti protein - mem |
| 13 | 85 | 14.0 | 385 | 2 | B84287 | calcium-binding pr |
| 14 | 84 | 13.8 | 785 | 2 | T09491 | hemagglutinin, pha |
| 15 | 84 | 13.8 | 1963 | 1 | MXKW | myosin heavy chain |
| 16 | 83.5 | 13.8 | 623 | 2 | S34440 | dnak-type molecula |
| 17 | 83.5 | 13.8 | 1621 | 2 | A82255 | hypothetical prote |
| 18 | 83 | 13.7 | 586 | 2 | S48755 | major surface prot |
| 19 | 83 | 13.7 | 732 | 2 | T32757 | hypothetical prote |
| 20 | 82.5 | 13.6 | 220 | 2 | T71980 | hypothetical prote |
| 21 | 82.5 | 13.6 | 2132 | 1 | A55182 | aggreccan precursor |
| 22 | 82 | 13.5 | 344 | 2 | A30544 | dnak-type molecula |
| 23 | 82 | 13.5 | 407 | 2 | F72343 | hypothetical prote |
| 24 | 82 | 13.5 | 425 | 2 | H83652 | seryl-tRNA synthet |
| 25 | 82 | 13.5 | 487 | 1 | F1BP74 | fibrinittin - phage T |
| 26 | 82 | 13.5 | 593 | 2 | H64529 | hypothetical prote |
| 27 | 82 | 13.5 | 620 | 2 | E87221 | 70 kD heat shock p |
| 28 | 82 | 13.5 | 2124 | 2 | A28452 | proteoglycan core |
| 29 | 81.5 | 13.4 | 1113 | 1 | R6FPF2 | acidic ribosomal p |

KW Pneumococcal surface protein A; PepA; diagnosis; antigenic; vaccine;
 XX immunological; gene therapy; immunostimulant.

Unidentified.

US6592876-B1.

PD 15-JUL-2003.

XX 15-SEP-1995; 95US-00529055.

XX 20-APR-1993; 93US-00048896.

PR 06-JUN-1995; 95US-00465746.

XX (UABR-) UAB RES FOUND.

XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX WPI; 2003-862841/80.

XX Immunological composition for obtaining expression products used for
 PT detecting the presence of Streptococcus pneumoniae or its strain,
 PT comprises at least two different full length isolated gene encoding
 PT pneumococcal surface protein A.

XX Example 6; SEQ ID NO 68; 121pp; English.

XX The present invention relates to an immunological composition comprising
 CC at least 2 different full length isolated genes encoding pneumococcal
 CC surface protein A (PspA) from different groups based on restriction
 CC fragment polymorphism analysis. The invention is useful for obtaining
 CC expression products by recombinant techniques to detect, determine,
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its
 CC strain. The expression product is useful for preparing antigenic,
 CC immunological or vaccine compositions, for eliciting antibodies, an
 CC immunological response (other than or additional to antibodies) or a
 CC protective response (including antibody or other immunological response
 CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is Bg7817c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention

SQ Sequence 212 AA;

Query Match 46.2%; Score 280.5; DB 7; Length 212;
 Best Local Similarity 51.3%; Pred. No. 6.8e-21;
 Matches 61; Conservative 18; Mismatches 29; Indels 11; Gaps 2;

QY 1 LEDSGIGLEKVLATLDPGETPDGLDKSEDSNIGALPNQVSDLENQVSELDREVTRLP 60

DB 28 LEKAGAGLGNLSTLDPGKTQDELDKEAAE---AELNKKVYALPNQVALEELSKLE 83

QY 61 SLDKDTGNNVGDYVKGLEKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119

DB 84 DNLKDAETHNVEDYIKGLEAIAIKQAELEKT-----PKELDALNELGPDGDEE 135

Search completed: November 17, 2005, 20:19:44
 Job time : 85.5636 secs

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QY      61  SLDKDTGNNVGDYVKGGLKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEEE 119
      :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      332  DNLKDAETNNVEDYIKEGLEEAIA TKAELEKT-----QKELDAALNELGPDGDEEE 383

RESULT 13
AAW14590
ID  AAW14590 standard; protein; 233 AA.
XX
AC  AAW14590;
XX
DT  17-OCT-2003 (revised)
DT  28-OCT-1997 (first entry)
XX
DE  Streptococcus pneumoniae PspA central region.
XX
KW  PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW  bacteraemia; pneumonia.
XX
OS  Streptococcus pneumoniae; strain Ef5668.
XX
PN  WO9709994-A1.
XX
PD  20-MAR-1997.
XX
PF  16-SEP-1996; 96WO-US014819.
XX
PR  15-SEP-1995; 95US-00529055.
XX
PA  (UABR-) UAB RES FOUND.
XX
PI  Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI  Hollingshead S, Tart R, Brooks-Walter A;
XX
DR  WPI; 1997-202002/18.
XX
PT  Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT  in vaccines for protecting animals against S.pneumoniae infection.
XX
PS  Example 6; Fig 13; 296pp; English.
XX
CC  This sequence shows the central portion, including the C-terminus of the
CC  alpha-helix region and some of the proline-rich region, of pneumococcal
CC  surface protein A (PspA) of Streptococcus pneumoniae strain Ef5668 (see
CC  also AAW14592). Comparison of the N-terminal and central regions
CC  (AAW14533-57 and AAW14562-91) of PspA from different pneumococcal strains
CC  can be used to divide the strains into several families based on sequence
CC  homologies. PspA polypeptides, or fragments of them, can be used in
CC  vaccines to protect animals against S. pneumoniae infection and hence for
CC  the prevention of diseases such as otitis media, meningitis, bacteraemia
CC  and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC  region and the immediate 5' tip of the coding sequence are likely to be
CC  the critical sequences for predicting PspA cross-reactions and vaccine
CC  composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ  Sequence 233 AA;

Query Match      47.4%; Score 288; DB 2; Length 233;
Best Local Similarity 55.0%; Pred. No. 1.3e-21;
Matches 66; Conservative 15; Mismatches 27; Indels 12; Gaps 3;

QY      1  LEDSLGLGKLVATLDP-GGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRL 59
      ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      51  LEDAELEKLVATLDPGEGKTQDELDEKAAE-----AELNEKVEALQNQVALEELSGL 106

QY      60  PSDLKDTEGNNVDYVKGGLKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEEE 119
      :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      107  EDNLKDAETNNVEDYIKEGLEEAIA TKAELEKT-----QKELDAALNELGPDGDEEE 159

RESULT 14
AAW14588
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```
ID  AAW14588 standard; protein; 212 AA.
XX
AC  AAW14588;
XX
DT  17-OCT-2003 (revised)
DT  28-OCT-1997 (first entry)
XX
DE  Streptococcus pneumoniae PspA central region.
XX
KW  PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW  bacteraemia; pneumonia.
XX
OS  Streptococcus pneumoniae; strain Bg7817.
XX
PN  WO9709994-A1.
XX
PD  20-MAR-1997.
XX
PF  16-SEP-1996; 96WO-US014819.
XX
PR  15-SEP-1995; 95US-00529055.
XX
PA  (UABR-) UAB RES FOUND.
XX
PI  Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI  Hollingshead S, Tart R, Brooks-Walter A;
XX
DR  WPI; 1997-202002/18.
XX
PT  Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT  in vaccines for protecting animals against S.pneumoniae infection.
XX
PS  Example 6; Fig 13; 296pp; English.
XX
CC  This sequence shows the central portion, including the C-terminus of the
CC  alpha-helix region and some of the proline-rich region, of pneumococcal
CC  surface protein A (PspA) of Streptococcus pneumoniae strain Bg7817.
CC  Comparison of the N-terminal and central regions (AAW14533-57 and
CC  AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC  be used to divide the strains into several families based on sequence
CC  homologies. PspA polypeptides, or fragments of them, can be used in
CC  vaccines to protect animals against S. pneumoniae infection and hence for
CC  the prevention of diseases such as otitis media, meningitis, bacteraemia
CC  and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC  region and the immediate 5' tip of the coding sequence are likely to be
CC  the critical sequences for predicting PspA cross-reactions and vaccine
CC  composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ  Sequence 212 AA;

Query Match      46.2%; Score 280.5; DB 2; Length 212;
Best Local Similarity 51.3%; Pred. No. 6.8e-21;
Matches 61; Conservative 18; Mismatches 29; Indels 11; Gaps 2;

QY      1  LEDSLGLGKLVATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDREVTRL 60
      ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      28  LEKAGAGLGNLSTLDPGKTQDELDEKAAE-----AELNKKVEALPNQVALEELSXL 83

QY      61  SLDKDTGNNVDYVKGGLKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEEE 119
      :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      84  DNLKDAETNNVEDYIKEGLEEAIA TKAELEKT-----PKELDAALNELGPDGDEEE 135

RESULT 15
ABW02622
ID  ABW02622 standard; protein; 212 AA.
XX
AC  ABW02622;
XX
DT  12-FEB-2004 (first entry)
XX
DE  Bg7817c pneumococcal surface protein A (PspA) central region.
XX
```


CC immunological or vaccine compositions, for eliciting antibodies, an
 CC immunological response (other than or additional to antibodies) or a
 CC protective response (including antibody or other immunological response
 CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is Ef5668 pneumococcal
 CC surface protein A (PspA) used in the exemplification of the invention
 XX
 SQ Sequence 458 AA;

Query Match 49.2%; Score 298.5; DB 7; Length 458;
 Best Local Similarity 55.5%; Pred. No. 2.5e-22;
 Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;
 QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
 Db 276 LEDAELEKVLATLDPGGTDPGLDKEAAE---AELNEKVEALQNVAELEELSKE 331
 QY 61 SLDKTEGNNVGVYKGLKALTDKVLGNNTPKALDTAPKALDTALNELGPDGDEE 119
 Db 332 DNLKDAETNNVEDYIKGLEEAIATKAELEKT-----QKELDALNELGPDGDEE 383

RESULT 11
 ADK52495
 ID ADK52495 standard; protein; 653 AA.
 AC ADK52495;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE PspA molecule from the Rx1 strain of Streptococcus pneumoniae.
 XX
 KW Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
 KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
 KW Hodgkin's disease.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO2004016231-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 17-FEB-2003; 2003WO-US008199.
 XX
 PR 15-MAR-2002; 2002US-0365351P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Briles DE;
 XX
 DR WPI; 2004-192068/18.
 XX
 PT Treating Streptococcus pneumoniae infection in a subject lacking a
 PT functional spleen comprises administering an antibody that recognizes
 PT pneumococcal surface protein A (PspA) or its binding portion.
 XX
 PS Claim 17; SEQ ID NO 1; 41pp; English.

CC The present invention relates to treating Streptococcus pneumoniae
 CC infection in a subject lacking a functional spleen comprises
 CC administering an antibody that recognizes pneumococcal surface protein A
 CC (PspA) or its binding portion. The method is useful for treating or
 CC preventing Streptococcus pneumoniae infection in a subject lacking a
 CC functional spleen. The disease-associated injury is especially due to
 CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
 CC anemia or Hodgkin's disease. The present sequence represents PspA
 CC molecule from the Rx1 strain of Streptococcus pneumoniae.
 XX
 SQ Sequence 653 AA;

Query Match 49.2%; Score 298.5; DB 8; Length 653;
 Best Local Similarity 55.5%; Pred. No. 4.1e-22;
 Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;

QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
 Db 276 LEDAELEKVLATLDPGGTDPGLDKEAAE---AELNEKVEALQNVAELEELSKE 331
 QY 61 SLDKTEGNNVGVYKGLKALTDKVLGNNTPKALDTAPKALDTALNELGPDGDEE 119
 Db 332 DNLKDAETNNVEDYIKGLEEAIATKAELEKT-----QKELDALNELGPDGDEE 383

RESULT 12
 ADOS2080
 ID ADOS2080 standard; protein; 653 AA.
 AC ADOS2080;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE S. pneumoniae strain EF5688 PspA protein.
 XX
 KW Immunogenic composition; vaccine; Th2-type immune response;
 KW pneumococcal surface protein A; PspA.
 XX
 OS Streptococcus pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT Protein /label= Signal_peptide
 FT Protein 32..653
 FT Domain /note= "S. pneumoniae strain EF5688 mature PspA protein"
 FT Domain 110..384
 FT Domain /note = PspA alpha-helical domain
 XX
 PN US2004101531-A1.
 XX
 PD 27-MAY-2004.
 XX
 PF 15-APR-2003; 2003US-00414532.
 XX
 PR 16-APR-2002; 2002US-0372710P.
 XX
 PA (CURT/) CURTISS R.
 PA (KANG/) KANG H Y.
 XX
 PI Curtiss R, Kang HY;
 XX
 DR WPI; 2004-399655/37.
 DR N-PSDB; ADO52067.
 XX
 PT New vaccine comprising a live attenuated strain of pathogenic gram-
 PT negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 PT or bacteria.
 XX
 PS Example 5; SEQ ID NO 26; 94pp; English.
 XX

Query Match 49.2%; Score 298.5; DB 8; Length 653;
 Best Local Similarity 55.5%; Pred. No. 4.1e-22;
 Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;
 QY 1 LEDSGLGLEKVLATLDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRLP 60
 Db 276 LEDAELEKVLATLDPGGTDPGLDKEAAE---AELNEKVEALQNVAELEELSKE 331

XX Briles DE;
PI WPI; 2004-192068/18.
DR
XX
XX Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX
XX Claim 17; SEQ ID NO 2; 41pp; English.
XX
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rx1 strain of Streptococcus
CC pneumoniae.
XX
XX Sequence 369 AA;
SQ

Query Match 49.2%; Score 298.5; DB 8; Length 369;
Best Local Similarity 55.5%; Pred. No. 1.9e-22;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;
QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
Db 245 LEDAELEKVLATLDPEGKTQDELDEKAAE----AELNEKVEALQNQVAELEELSLE 300
QY 61 SLDKTEGNNVGDYVKGGLKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119
Db 301 DNLKDAETNNVEDYIKEGLEEAIAIKAELEKT-----QKELDAALNELGPDGDEE 352

RESULT 9
AAW14592
ID AAW14592 standard; protein; 458 AA.
XX
XX AAW14592;
XX
XX 17-OCT-2003 (revised)
DT 27-OCT-1997 (first entry)
XX
XX Streptococcus pneumoniae PspA surface protein.
DE
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
KW
XX Streptococcus pneumoniae; strain Ef5668.
OS
XX WO9709994-A1.
PN
XX
XX 20-MAR-1997.
PD
XX
XX 16-SEP-1996; 96WO-US014819.
PF
XX
XX 15-SEP-1995; 95US-00529055.
PR
XX (UABR-) UAB RES FOUND.
PA
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
PI
XX WPI; 1997-202002/18.
DR
XX N-PSDB; AAT61724.
DR
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
PT
XX Disclosure; Fig 13; 296pp; English.
PS

XX This sequence comprises the pneumococcal surface protein A (pspA) of
CC Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the
CC pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be
CC used in vaccines to protect animals against S. pneumoniae infection and
CC hence for the prevention of diseases such as otitis media, meningitis,
CC bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 458 AA;
SQ

Query Match 49.2%; Score 298.5; DB 2; Length 458;
Best Local Similarity 55.5%; Pred. No. 2.5e-22;
Matches 66; Conservative 15; Mismatches 27; Indels 11; Gaps 2;
QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASEDSNIGALPNQVSDLENQVSELDREVTRLP 60
Db 276 LEDAELEKVLATLDPEGKTQDELDEKAAE----AELNEKVEALQNQVAELEELSLE 331
QY 61 SLDKTEGNNVGDYVKGGLKALTDEKVLNNTPKALDTAPKALDTALNELGPDGDEE 119
Db 332 DNLKDAETNNVEDYIKEGLEEAIAIKAELEKT-----QKELDAALNELGPDGDEE 383

RESULT 10
ABW02626
ID ABW02626 standard; protein; 458 AA.
XX
XX ABW02626;
AC
XX 12-FEB-2004 (first entry)
DT
XX Ef5668 pneumococcal surface protein A (PspA).
DE
XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
KW
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 458
FT /note= "Encoded by GC"
FT
XX US6592876-B1.
PN
XX 15-JUL-2003.
PD
XX 15-SEP-1995; 95US-00529055.
PF
XX 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
PR
XX (UABR-) UAB RES FOUND.
PA
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
PI
XX WPI; 2003-862841/80.
DR N-PSDB; AAD64535.
DR
XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
PT
XX Example 6; SEQ ID NO 73; 121pp; English.
PS
XX The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC


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QY 61  SLDKTEGNNVGDYVKGGLKALTDKVGGLNTPKALDTAPKALDTALNELGPDGDEE 119
Db 87  SLDKTEGNNVGDYVKGGLKALTDKVGGLNTPKALDTAPKALDTALNELGPDGDEE 145

RESULT 4
ABU08487
ID  ABU08487 standard; protein; 8991 AA.
XX  AC
XX  ABU08487;
DT  24-JUN-2003 (first entry)
XX  XX
DE  S. pneumoniae pneumococcal surface protein A (PspA) protein.
KW  Pneumococcal surface protein C; PspC; pneumococcal surface protein A;
KW  alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;
KW  antibacterial.
XX  XX
OS  Streptococcus pneumoniae.
XX  XX
FH  Key Location/Qualifiers
FT  Misc-difference 1..8991
FT  /note="All Xaa residues within this sequence are
FT  unknown"
FT  FT
XX  US6500613-B1.
XX  31-DEC-2002.
XX  XX
PF  16-SEP-1996; 96US-00714741.
XX  XX
PR  15-SEP-1995; 95US-00529055.
XX  XX
PA  (UYAL-) UNIV ALABAMA.
XX  XX
PI  Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI  Hollingshead S, Tart R, Brooks-Walter A;
XX  WPI; 2003-361534/34.
XX  XX
XX  Isolated PspC amino acid sequence used as polymerase chain reaction or
PT  hybridization probe, comprises pneumococcal surface protein having alpha-
PT  helical, proline rich and repeat regions.
XX  XX
PS  Disclosure; Col 145-188; 186pp; English.
XX  XX
CC  The present invention relates to the isolation of Streptococcus
CC  pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide
CC  sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-
CC  like protein having alpha-helical, proline rich and repeat regions. The
CC  PspC and PspA proteins may be used in a vaccine to protect against
CC  pneumococcal infections. The polynucleotide sequences encoding PspC and
CC  PspA may be used for the expression of the proteins, and as PCR primers
CC  or hybridisation probes. The present sequence represents S. pneumoniae
CC  PspA protein
XX  XX
SQ  Sequence 8991 AA;

Query Match 100.0%; Score 607; DB 6; Length 8991;
Best Local Similarity 100.0%; Pred. No. 7.7e-53;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRL 60
Db 3874 LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRL 3933

QY 61  SLDKTEGNNVGDYVKGGLKALTDKVGGLNTPKALDTAPKALDTALNELGPDGDEE 119
Db 3934 SLDKTEGNNVGDYVKGGLKALTDKVGGLNTPKALDTAPKALDTALNELGPDGDEE 3992

RESULT 5
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ADO15316
ID  ADO15316 standard; protein; 459 AA.
XX  AC
XX  ADO15316;
DT  12-AUG-2004 (first entry)
XX  XX
DE  S_pneumoniae pneumolysin protein encoded by pSA-60 PspA SeqID 18.
KW  pneumococcal infection; capsular protein; pneumolysin; vaccine;
KW  immunostimulant; antibacterial; mutant; mutein.
XX  XX
OS  Streptococcus pneumoniae.
OS  Synthetic.
XX  XX
PN  WO2004043376-A2.
XX  27-MAY-2004.
XX  XX
PF  06-NOV-2003; 2003WO-US035529.
XX  XX
PR  07-NOV-2002; 2002US-0424497P.
XX  XX
PA  (SYNE-) SYNERGY AMERICA INC.
XX  XX
PI  Chen MC, Chiou C, Li Z, Chen D;
XX  WPI; 2004-411623/38.
XX  N-PSDB; ADO15315.
XX  XX
PT  New compositions comprising a polypeptide conjugated to Streptococcus
PT  pneumoniae capsular polysaccharide or non-S. pneumoniae bacterial
PT  polysaccharide, useful for eliciting an immune response against S.
PT  pneumoniae.
XX  XX
PS  Claim 51; SEQ ID NO 18; 69pp; English.
XX  XX
CC  This invention relates to novel proteins and polypeptide conjugates that
CC  can be used to treat and/or prevent pneumococcal infections.
CC  Specifically, it refers to compositions that preferably contain a
CC  polypeptide conjugated to a Streptococcus pneumoniae (S. pneumoniae)
CC  capsular protein such as the pneumolysin protein that has been modified
CC  to lack the peptide sequence Lys-Val-Glu-Asn-Asp and hence also lack
CC  haemolytic activity. The present invention describes such compositions as
CC  useful for eliciting a cellular or humoral immune response against S.
CC  pneumoniae when administered to a mammal, and further provides antibodies
CC  useful for the development of vaccines to treat and/or prevent
CC  pneumococcal infection. Accordingly, these compositions are
CC  immunostimulants and exhibit antibacterial activities. This polypeptide
CC  sequence is the protein encoded by the S. pneumoniae pneumolysin pSA-60
CC  PspA expression vector of the invention.
XX  XX
SQ  Sequence 459 AA;

Query Match 71.2%; Score 432; DB 8; Length 459;
Best Local Similarity 77.4%; Pred. No. 2.7e-36;
Matches 89; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1  LEDSGLGLEKVLATDPGGTDPGLDKEASDSNIGALPNQVSDLENQVSELDREVTRL 60
Db 345 LEDAELEKVLATLDPGGTQDQLDKEAEDANIEALQNKVADLENKVAELDKVTRLQ 404

QY 61  SLDKTEGNNVGDYVKGGLKALTDKVGGLNTPKALDTAPKALDTALNELGPDG 115
Db 405 SLDKDAENNVGDYVKGGLKALTDKVELANTQKALDTAOKALDTALNELGPDG 459

RESULT 6
ABW02624
ID  ABW02624 standard; protein; 232 AA.
XX  AC
XX  ABW02624;
```

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QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 60
Db 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 60
QY 61 SDLKDTGNNVGDYVKGGLKALTDKVKGLNNTPKALDTAPKALDTALNELGPDGDEE 119
Db 61 SDLKDTGNNVGDYVKGGLKALTDKVKGLNNTPKALDTAPKALDTALNELGPDGDEE 119

RESULT 2
AAW14563
ID AAW14563 standard; protein; 215 AA.
XX
AC AAW14563;
XX
DT 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain ATCC 6303.
XX
FH Key Location/Qualifiers
FT Misc-difference 4
FT /note= "unidentified amino acid"
FT Misc-difference 16
FT /note= "unidentified amino acid"
XX
PN WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
DR WPI; 1997-202002/18.
XX
PS Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
XX
XX Example 6; Fig 13; 296pp; English.
XX
This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain ATCC6303.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 607; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 60
Db 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 60
```

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Db 27 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 86
QY 61 SDLKDTGNNVGDYVKGGLKALTDKVKGLNNTPKALDTAPKALDTALNELGPDGDEE 119
Db 87 SDLKDTGNNVGDYVKGGLKALTDKVKGLNNTPKALDTAPKALDTALNELGPDGDEE 145

RESULT 3
ABW02597
ID ABW02597 standard; protein; 215 AA.
XX
AC ABW02597;
XX
DT 12-FEB-2004 (first entry)
XX
DE Atcc6303c pneumococcal surface protein A (PspA) central region.
XX
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..215
FT /note= "Xaa = Unknown amino acid"
XX
PN US6592876-B1.
XX
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
PI WPI; 2003-862841/80.
XX
XX Immunological composition for obtaining expression products used for
XX detecting the presence of Streptococcus pneumoniae or its strain,
XX comprises at least two different full length isolated gene encoding
XX pneumococcal surface protein A.
XX
XX Example 6; SEQ ID NO 43; 121pp; English.
XX
The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Atcc6303c
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 607; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 60
Db 27 LEDSGLGLEKVLATLDPGGETPDGLDKEASDSNIGALPNQVSDLENQVSELDRVTRLP 86
```

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 84.5636 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-27

Perfect score: 607

Sequence: 1 LEDSGLGLEKVLATLDPGGE.....APKALDTALNELGPDGDEE 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 607 | 100.0 | 119 | 2 | AAW46291 Pneumoc |
| 2 | 607 | 100.0 | 215 | 2 | AAW14563 Streptoco |
| 3 | 607 | 100.0 | 215 | 7 | ABW02597 Atcc6303c |
| 4 | 607 | 100.0 | 8991 | 6 | ABU08487 S. pneumo |
| 5 | 432 | 71.2 | 459 | 8 | ADO15316 S. pneumon |
| 6 | 298.5 | 49.2 | 232 | 7 | ABW02624 Ef5668c p |
| 7 | 298.5 | 49.2 | 269 | 8 | ADO52055 S. pneumo |
| 8 | 298.5 | 49.2 | 375 | 8 | ADK52496 alpha hel |
| 9 | 298.5 | 49.2 | 458 | 2 | AAW14592 Streptoco |
| 10 | 298.5 | 49.2 | 458 | 7 | ABW02626 Ef5668 pn |
| 11 | 298.5 | 49.2 | 653 | 8 | ADK52495 PspA mole |
| 12 | 298.5 | 49.2 | 653 | 8 | ADO52080 S. pneumo |
| 13 | 288 | 47.4 | 233 | 2 | AAW14590 Streptoco |
| 14 | 280.5 | 46.2 | 212 | 2 | AAW14588 Streptoco |
| 15 | 280.5 | 46.2 | 212 | 7 | ABW02622 Bg7817c p |
| 16 | 279.5 | 46.0 | 211 | 7 | ABW02621 Bg11703c |
| 17 | 279.5 | 46.0 | 238 | 2 | AAW14587 Streptoco |
| 18 | 228.5 | 37.6 | 185 | 7 | ABW02623 Bg7561c p |
| 19 | 205 | 33.8 | 184 | 2 | AAW14589 Streptoco |
| 20 | 200.5 | 33.0 | 233 | 7 | ABW02606 Bf1019c p |
| 21 | 199 | 32.8 | 230 | 8 | ADO52086 S. pneumo |
| 22 | 199 | 32.8 | 230 | 8 | ADR04319 Streptoco |
| 23 | 199 | 32.8 | 290 | 8 | ADO52119 pYA3637 b |
| 24 | 199 | 32.8 | 298 | 8 | ADO52127 pYA3637 b |
| 25 | 199 | 32.8 | 487 | 8 | ADR04321 Streptoco |

| | | | | | | |
|----|-------|------|------|---|----------|---------------------|
| 26 | 199 | 32.8 | 489 | 8 | ADO52088 | Ado52088 Streptoco |
| 27 | 199 | 32.8 | 524 | 8 | ADO52082 | Ado52082 E. coli B |
| 28 | 199 | 32.8 | 627 | 8 | ADO52129 | Ado52129 E. coli B |
| 29 | 196.5 | 32.4 | 213 | 7 | ABW02601 | Abw02601 Bg8090c p |
| 30 | 193.5 | 31.9 | 233 | 2 | AAW14572 | Aaw14572 Streptoco |
| 31 | 190.5 | 31.4 | 197 | 7 | ABW02598 | Abw02598 Ac122c pn |
| 32 | 190.5 | 31.4 | 416 | 8 | ADK52498 | Adk52498 alpha hel |
| 33 | 190.5 | 31.4 | 526 | 8 | ADK52497 | Adk52497 PspA mole |
| 34 | 190.5 | 31.4 | 744 | 6 | ABU00449 | Abu00449 S. pneumo |
| 35 | 190.5 | 31.4 | 744 | 8 | ADM92054 | Adm92054 S. pneumon |
| 36 | 190.5 | 31.4 | 745 | 3 | AAW14562 | Aay81452 Streptoco |
| 37 | 189.5 | 31.2 | 641 | 2 | AAW61217 | Aaw61217 Streptoco |
| 38 | 189.5 | 31.2 | 641 | 5 | ABP54636 | Abp54636 S. pneumo |
| 39 | 189.5 | 31.2 | 641 | 7 | ADC45241 | Adc45241 S. pneumo |
| 40 | 185.5 | 30.6 | 213 | 2 | AAW14567 | Aaw14567 Streptoco |
| 41 | 179 | 29.5 | 196 | 2 | AAW14564 | Aaw14564 Streptoco |
| 42 | 114.5 | 18.9 | 1231 | 6 | ABU08490 | Abu08490 Fragment |
| 43 | 114 | 18.8 | 289 | 2 | AAW62276 | Aaw62276 Streptoco |
| 44 | 114 | 18.8 | 289 | 2 | AAW11840 | Aay411840 Streptoco |
| 45 | 114 | 18.8 | 289 | 2 | AAW87910 | Aaw87910 Protein s |

ALIGNMENTS

RESULT 1
AAW46291
ID AAW46291 standard; protein; 119 AA.

AC AAW46291;

DT 29-JUL-1998 (first entry)

DE Pneumococcal surface protein As (PspAs) from clade 5 strain ATCC6303.

XX Streptococcus pneumoniae; vaccine; pneumococcal surface protein As;

KW infection; protection; PspAs.

XX Streptococcus pneumoniae.

XX WO9811915-Al.

XX 26-MAR-1998.

PF 22-SEP-1997; 97WO-US016761.

PR 20-SEP-1996; 96US-00710749.

XX (CONN-) CONNAUGHT LAB LTD.

XX Becker RS, Briles DE, Hollingshead S;

DR WPI; 1998-217031/19.

XX New vaccines for protection against pneumococcal infection - comprising at least 2 pneumococcal surface protein As, each selected from a different family.

PS Example 3; Fig 7; 57pp; English.

XX This is the sequence of a pneumococcal surface protein As (PspAs) from strain ATCC6303, a representative strain of clade 5. This can be used in the preparation of a vaccine composition comprising at least 2 PspAs, each of which is selected from a different family. The vaccines can provide for broad range protection against infection by different Streptococcus pneumoniae strains

XX Sequence 119 AA;

Query Match 100.0%; Score 607; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2.2e-55;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide of pSA-60 PapA insert sequence
US-10-702-305A-18

Query Match          52.0%; Score 281; DB 16; Length 459;
Best Local Similarity 53.5%; Pred. No. 1.6e-16;
Matches 61; Conservative 14; Mismatches 25; Indels 14; Gaps 1;

QY 1 LKAAEAELENLLSTLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 54
Db 232 LAKKQTELEKLLDNLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 54
QY 55 -----PEDNLKDAETNHVEDYIKEGLEEAATKQAELEETPQEVDAALNDL 100
Db 292 ELNKEIARLQSDLKDAEENNVEDYIKEGLEQAIAADKKAEALATTQQNIDTKQKDL 345

RESULT 14
US-10-299-636-62
; Sequence 62, Application US/10299636
; Publication No. US2004007847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa at position 2 is unknown
US-10-299-636-62

Query Match          50.0%; Score 270; DB 15; Length 213;
Best Local Similarity 51.3%; Pred. No. 5.8e-16;
Matches 60; Conservative 13; Mismatches 22; Indels 22; Gaps 2;

QY 1 LKAAEAELENLLSTLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 53
Db 59 LAKKQTELEKLLDNLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 53
QY 54 --PPEDNLKDAETNHVEDYIKEGLEEAATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 119 GADPEDD-----TAAALPNKLTATKKAEEKTPKELDAALNELGPDGDEE 162

RESULT 15
US-10-674-755-21
; Sequence 21, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
```

```
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-21

Query Match          49.3%; Score 266; DB 15; Length 104;
Best Local Similarity 51.3%; Pred. No. 5.5e-16;
Matches 60; Conservative 13; Mismatches 22; Indels 22; Gaps 2;

QY 1 LKAAEAELENLLSTLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 53
Db 1 LAKKQTELEKLLDNLDPGKQTODELDKGAEEAELENKKVEALPNPYXELBEELS----- 53
QY 54 --PPEDNLKDAETNHVEDYIKEGLEEAATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 61 GADPEDD-----TAAALPNKLTATKKAEEKTPKELDAALNELGPDGDEE 104

Search completed: November 17, 2005, 20:29:19
Job time : 71.832 secs
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Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 LEKAAELENLSTLDPGGKTODELDKGAAEALNKKVEALPNPVXELBEELSPPEDNLK 60
|||||
Db 1 LEKAGAGLNLSTLDPEGKTODELDKEAAEALNKKVEALPNQVAELBEELSLEDNLK 60
QY 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
|||||
Db 61 DAETHNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108

RESULT 6
US-10-299-636-83
; Sequence 83, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-83

Query Match 82.8%; Score 447; DB 15; Length 212;
Best Local Similarity 86.1%; Pred. No. 1.3e-31;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 LEKAAELENLSTLDPGGKTODELDKGAAEALNKKVEALPNPVXELBEELSPPEDNLK 60
|||||
Db 28 LEKAGAGLNLSTLDPEGKTODELDKEAAEALNKKVEALPNQVAELBEELSLEDNLK 87
QY 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 88 DAETHNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 135

RESULT 7
US-10-674-755-22
; Sequence 22, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-22

Query Match 81.3%; Score 439; DB 15; Length 106;
Best Local Similarity 88.0%; Pred. No. 2.8e-31;
Matches 95; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
QY 1 LEKAAELENLSTLDPGGKTODELDKGAAEALNKKVEALPNPVXELBEELSPPEDNLK 60
|||||
Db 1 LEKAAELENLSTLDPEGKTODELDKEAAEALNKKVEALPNQV-ELBEELSLEDNLK 59
QY 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
|||||
Db 60 DAETHN-VEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 106

RESULT 8
US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-25

Query Match 76.7%; Score 414; DB 15; Length 108;
Best Local Similarity 79.6%; Pred. No. 4.7e-29;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 1 LEKAAELENLSTLDPGGKTODELDKGAAEALNKKVEALPNPVXELBEELSPPEDNLK 60
|||||
Db 1 LEDAELEKVLATLDPEGKTODELDKEAAEALNKKVEALQNQVAELBEELSLEDNLK 60
QY 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
|||||
Db 61 DAETHNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108

RESULT 9
US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-85

Db 61 DAETNHVEDYIKGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGEEE 108

RESULT 2

US-10-299-636-84

; Sequence 84, Application US/10299636

; Publication No. US20040077847A1

; GENERAL INFORMATION:

; APPLICANT: Briles, David E

; APPLICANT: McDaniel, Larry S

; APPLICANT: Swiatlo, Edwin

; APPLICANT: Yother, Janet

; APPLICANT: Crain, Marilyn J

; APPLICANT: Hollingshead, Susan

; APPLICANT: Tart, Rebecca

; APPLICANT: Brooks-Walter, Alexis

; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF

; FILE REFERENCE: 57909/361

; CURRENT APPLICATION NUMBER: US/10/299,636

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: 08/714,741

; PRIOR FILING DATE: 1996-09-16

; PRIOR APPLICATION NUMBER: 08/529,055

; PRIOR FILING DATE: 1995-09-15

; NUMBER OF SEQ ID NOS: 111

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 84

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

; NAME/KEY: UNSURE

; LOCATION: (45)

; OTHER INFORMATION: Xaa at position 45 is unknown

US-10-299-636-84

Query Match 94.8%; Score 512; DB 15; Length 185;

Best Local Similarity 95.3%; Pred. No. 1.9e-37;

Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKAAELENLLSTLDPGGKTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLKD 61

Db 1 KQQVNLNLLSTLDPGGKTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLKD 60

Qy 62 AETNHVEDYIKGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGEEE 108

Db 61 AETNHVEDYIKGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGEEE 107

RESULT 3

US-10-674-755-23

; Sequence 23, Application US/10674755

; Publication No. US20040067237A1

; GENERAL INFORMATION:

; APPLICANT: BECKER et al.

; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

; FILE REFERENCE: 454312-2471

; CURRENT APPLICATION NUMBER: US/10/674,755

; CURRENT FILING DATE: 2003-09-30

; PRIOR APPLICATION NUMBER: US/09/147,875A

; PRIOR FILING DATE: 1999-05-24

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-674-755-23

Query Match 85.4%; Score 461; DB 15; Length 108;

Best Local Similarity 88.0%; Pred. No. 3.3e-33;

Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LEKAAELENLLSTLDPGGKTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLK 60

Db 1 LEKAAELENLLSTLDPGGKTQDELKGAAEALNKKVEALPNPVXEELEELSKLEDNLK 60

Qy 61 DAETNHVEDYIKGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGEEE 108

Db 61 DAETNNVEDYIKGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 4

US-10-299-636-82

; Sequence 82, Application US/10299636

; Publication No. US20040077847A1

; GENERAL INFORMATION:

; APPLICANT: Briles, David E

; APPLICANT: McDaniel, Larry S

; APPLICANT: Swiatlo, Edwin

; APPLICANT: Yother, Janet

; APPLICANT: Crain, Marilyn J

; APPLICANT: Hollingshead, Susan

; APPLICANT: Tart, Rebecca

; APPLICANT: Brooks-Walter, Alexis

; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF

; FILE REFERENCE: 57909/361

; CURRENT APPLICATION NUMBER: US/10/299,636

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: 08/714,741

; PRIOR FILING DATE: 1996-09-16

; PRIOR APPLICATION NUMBER: 08/529,055

; PRIOR FILING DATE: 1995-09-15

; NUMBER OF SEQ ID NOS: 111

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 82

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-299-636-82

Query Match 85.4%; Score 461; DB 15; Length 211;

Best Local Similarity 88.0%; Pred. No. 7.4e-33;

Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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Db 25 LEKAAELENLLSTLDPGGKTQDELKGAAEALNKKVEALPNPVXEELEELSKLEDNLK 84

Qy 61 DAETNHVEDYIKGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGEEE 108

Db 85 DAETNNVEDYIKGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 132

RESULT 5

US-10-674-755-24

; Sequence 24, Application US/10674755

; Publication No. US20040067237A1

; GENERAL INFORMATION:

; APPLICANT: BECKER et al.

; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS

; FILE REFERENCE: 454312-2471

; CURRENT APPLICATION NUMBER: US/10/674,755

; CURRENT FILING DATE: 2003-09-30

; PRIOR APPLICATION NUMBER: US/09/147,875A

; PRIOR FILING DATE: 1999-05-24

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-674-755-24

Query Match 84.1%; Score 454; DB 15; Length 108;

Best Local Similarity 87.0%; Pred. No. 1.4e-32;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 71.832 Seconds
(without alignments)
629.082 Million cell updates/sec

Title: US-10-674-755-26
Perfect score: 540
Sequence: 1 LEKAELENLSTLDPGK.....TPQEVDAALNDLVPDGGSEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
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| 2 | 512 | 94.8 | 185 | 15 | US-10-299-636-84 |
| 3 | 461 | 85.4 | 108 | 15 | US-10-674-755-23 |
| 4 | 461 | 85.4 | 211 | 15 | US-10-299-636-82 |
| 5 | 454 | 84.1 | 108 | 15 | US-10-674-755-24 |
| 6 | 447 | 82.8 | 212 | 15 | US-10-299-636-83 |
| 7 | 439 | 81.3 | 106 | 15 | US-10-674-755-22 |
| 8 | 414 | 76.7 | 108 | 15 | US-10-674-755-25 |
| 9 | 414 | 76.7 | 232 | 15 | US-10-299-636-85 |
| 10 | 414 | 76.7 | 275 | 16 | US-10-414-532-1 |
| 11 | 414 | 76.7 | 458 | 15 | US-10-299-636-88 |

| | | | | | | |
|----|-------|------|-----|----|----------------------|--------------------|
| 12 | 414 | 76.7 | 653 | 16 | US-10-414-532-26 | Sequence 26, Appl |
| 13 | 281 | 52.0 | 459 | 16 | US-10-702-305A-18 | Sequence 18, Appl |
| 14 | 270 | 50.0 | 213 | 15 | US-10-299-636-62 | Sequence 62, Appl |
| 15 | 266 | 49.3 | 104 | 15 | US-10-674-755-21 | Sequence 21, Appl |
| 16 | 263 | 48.7 | 104 | 15 | US-10-674-755-20 | Sequence 20, Appl |
| 17 | 258 | 47.8 | 744 | 10 | US-09-789-787-184 | Sequence 184, Appl |
| 18 | 258 | 47.8 | 744 | 17 | US-10-472-928-32 | Sequence 32, Appl |
| 19 | 257 | 47.6 | 641 | 9 | US-09-765-272-160 | Sequence 160, Appl |
| 20 | 257 | 47.6 | 641 | 20 | US-11-106-649-160 | Sequence 160, Appl |
| 21 | 254 | 47.0 | 197 | 15 | US-10-299-636-59 | Sequence 59, Appl |
| 22 | 245 | 45.4 | 487 | 16 | US-10-414-532-34 | Sequence 34, Appl |
| 23 | 245 | 45.4 | 487 | 16 | US-10-414-533-21 | Sequence 21, Appl |
| 24 | 245 | 45.4 | 524 | 16 | US-10-414-532-28 | Sequence 28, Appl |
| 25 | 244 | 45.2 | 233 | 15 | US-10-299-636-67 | Sequence 67, Appl |
| 26 | 243 | 45.0 | 102 | 15 | US-10-674-755-18 | Sequence 18, Appl |
| 27 | 238 | 44.1 | 230 | 16 | US-10-414-532-32 | Sequence 32, Appl |
| 28 | 238 | 44.1 | 230 | 16 | US-10-414-533-19 | Sequence 19, Appl |
| 29 | 238 | 44.1 | 290 | 16 | US-10-414-532-65 | Sequence 65, Appl |
| 30 | 231.5 | 42.9 | 119 | 15 | US-10-674-755-27 | Sequence 27, Appl |
| 31 | 231.5 | 42.9 | 215 | 15 | US-10-299-636-58 | Sequence 58, Appl |
| 32 | 186 | 34.4 | 80 | 15 | US-10-674-755-19 | Sequence 19, Appl |
| 33 | 167 | 30.9 | 204 | 15 | US-10-299-636-66 | Sequence 66, Appl |
| 34 | 167 | 30.9 | 354 | 15 | US-10-299-636-105 | Sequence 105, Appl |
| 35 | 167 | 30.9 | 588 | 15 | US-10-299-636-96 | Sequence 96, Appl |
| 36 | 167 | 30.9 | 619 | 10 | US-09-882-774-1 | Sequence 1, Appl |
| 37 | 167 | 30.9 | 619 | 15 | US-10-282-122A-73702 | Sequence 73702, A |
| 38 | 167 | 30.9 | 619 | 16 | US-10-414-532-72 | Sequence 72, Appl |
| 39 | 164 | 30.4 | 99 | 15 | US-10-674-755-11 | Sequence 11, Appl |
| 40 | 160.5 | 29.7 | 100 | 15 | US-10-674-755-12 | Sequence 12, Appl |
| 41 | 159 | 29.4 | 198 | 15 | US-10-299-636-76 | Sequence 76, Appl |
| 42 | 143 | 26.5 | 195 | 15 | US-10-299-636-86 | Sequence 86, Appl |
| 43 | 139 | 25.7 | 99 | 15 | US-10-674-755-13 | Sequence 13, Appl |
| 44 | 139 | 25.7 | 141 | 14 | US-10-254-995-2 | Sequence 2, Appl |
| 45 | 139 | 25.7 | 336 | 15 | US-10-299-636-103 | Sequence 103, Appl |

ALIGNMENTS

RESULT 1
US-10-674-755-26
; Sequence 26, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(108)
; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
US-10-674-755-26

| | | | | |
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| Query Match | 99.6% | Score 538 | DB 15 | Length 108 |
| Best Local Similarity | 100.0% | Pred. No. 5.1e-40 | | |
| Matches 108 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| Qy | 1 | LEKAELENLSTLDPGKTTQDELKGAFAELNKKVEALPNPVXLEELSPEDNLK 60 | | |
| Db | 1 | LEKAELENLSTLDPGKTTQDELKGAFAELNKKVEALPNPVXLEELSPEDNLK 60 | | |
| Qy | 61 | DAETHVVEDYIKEGLEFAIATKQAELEETPQEVDAALNDLVPDGGSEE 108 | | |

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; MOLECULE TYPE: amino acid
US-08-710-749-24

Query Match
Best Local Similarity 76.7%; Score 414; DB 2; Length 108;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

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QY 61 DAETHNVEDYIKEGLEEAIAATKQAELETPQVDAALNDLVPDGGEEE 108
  ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELETKQKELDAALNDELPGDGDDEE 108
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RESULT 14
US-09-147-875A-25
; Sequence 25, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT.
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-25

Query Match
Best Local Similarity 76.7%; Score 414; DB 4; Length 108;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

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Db 1 LEDAELEKVLATLDPEGKTQDELKGAAEALNKKVEALQNVAAELEEELSKLEDNLK 60
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QY 61 DAETHNVEDYIKEGLEEAIAATKQAELETPQVDAALNDLVPDGGEEE 108
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Db 61 DAETNNVEDYIKEGLEEAIAATKQAELETKQKELDAALNDELPGDGDDEE 158
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-70

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Db 111 DAETNNVEDYIKEGLEEAIAATKQAELETKQKELDAALNDELPGDGDDEE 158
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US-08-529-055-70
; Sequence 70, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESS: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 15
US-08-529-055-70
; Sequence 70, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESS: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-67

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Best Local Similarity 88.0%; Pred. No. 2.6e-39;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

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Db 85 DAETHVVEDYIKGLEEAEIATKQAELEETPKELDAALNELGPDGDEEE 132

RESULT 8
US-09-147-875A-24
; Sequence 24, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-24

Query Match      84.1%; Score 454; DB 4; Length 108;
Best Local Similarity 87.0%; Pred. No. 5.8e-39;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LEKAEAELENLLSTLDPGKQTQDELKGAEEAEELNKKVEALPNPVKXEEELSPEDNLK 60
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RESULT 9
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-22

Query Match      82.8%; Score 447; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 3e-38;
Matches 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Db 1 LEKAGAGLENNLLSTLDPGKQTQDELKGAEEAEELNKKVEALPNQVSEELSKLEDNLK 60
Qy 61 DAETHVVEDYIKGLEEAEIATKQAELEETPOEVDAALNDLVPDGGEEE 108
Db 61 DAETHVVEDYIKGLEEAEIATKQAELEETPKELDAALNELGPDGDEEE 108

RESULT 10
US-08-710-749-23
; Sequence 23, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-23
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; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match          94.8%; Score 512; DB 4; Length 8991;
Best Local Similarity 95.3%; Pred. No. 2e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8380 KQKVNLENLLSTLDPGGKTQDELKGAABAELENKKVEALPNPVXEELEELSPEDNLK 8439

QY 62 AETNHVEDYIKGLEEAIAATKQAELEETPQEVDAALNDLVPDGGEE 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8440 AETNHVEDYIKGLEEAIAATKQAELEETPQEVDAALNDLVPDGGEE 8486

RESULT 5
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match          85.4%; Score 461; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.1e-39;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGGKTQDELKGAABAELENKKVEALPNPVXEELEELSPEDNLK 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 LEKAAELENLLSTLDPGGKTQDELKGAABAELENKKVEALPNPVXEELEELSKLEDNLK 60

QY 61 DAETNHVEDYIKGLEEAIAATKQAELEETPQEVDAALNDLVPDGGEE 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DAETNHVEDYIKGLEEAIAATKQAELEETPKELDAALNELPGDGGEE 108

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RESULT 6
US-09-147-875A-23
; Sequence 23, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-23

Query Match          85.4%; Score 461; DB 4; Length 108;
Best Local Similarity 88.0%; Pred. No. 1.1e-39;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGGKTQDELKGAABAELENKKVEALPNPVXEELEELSPEDNLK 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 LEKAAELENLLSTLDPGGKTQDELKGAABAELENKKVEALPNPVXEELEELSKLEDNLK 60

QY 61 DAETNHVEDYIKGLEEAIAATKQAELEETPQEVDAALNDLVPDGGEE 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 DAETNHVEDYIKGLEEAIAATKQAELEETPKELDAALNELPGDGGEE 108

RESULT 7
US-08-529-055-67
; Sequence 67, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid

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| Qy | 61 | DAETHNVEDYIKEGLEAEAIATKQAELEETPOEVDAALNDLVPDGGEEE | 108 |
| Db | 61 | DAETHNVEDYIKEGLEAEAIATKQAELEETPOEVDAALNDLVPDGGEEE | 108 |
| RESULT 2 | | | |
| US-09-147-875A-26 | | | |
| ; Sequence 26, Application US/09147875A | | | |
| ; Patent No. 6638516 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: BECKER et al. | | | |
| ; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS | | | |
| ; FILE REFERENCE: 454312-2471 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/147,875A | | | |
| ; CURRENT FILING DATE: 1999-05-24 | | | |
| ; NUMBER OF SEQ ID NOS: 28 | | | |
| ; SOFTWARE: PatentIn Ver. 2.1 | | | |
| ; SEQ ID NO 26 | | | |
| ; LENGTH: 108 | | | |
| ; TYPE: PRT | | | |
| ; ORGANISM: Streptococcus pneumoniae | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: UNSURE | | | |
| ; LOCATION: (1)..(108) | | | |
| ; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid | | | |
| US-09-147-875A-26 | | | |
| Query Match 99.6%; Score 538; DB 4; Length 108; | | | |
| Best Local Similarity 100.0%; Pred. No. 1.6e-47; Indels 0; Gaps 0; | | | |
| Matches 108; Conservative 0; Mismatches 0; | | | |
| Qy | 1 | LEKAAELENLSTLDPGKTKQDELDKGAAEALNKKVEALPNPVXLEBELSPEDNLK | 60 |
| Db | 1 | LEKAAELENLSTLDPGKTKQDELDKGAAEALNKKVEALPNPVXLEBELSPEDNLK | 60 |
| Qy | 61 | DAETHNVEDYIKEGLEAEAIATKQAELEETPOEVDAALNDLVPDGGEEE | 108 |
| Db | 61 | DAETHNVEDYIKEGLEAEAIATKQAELEETPOEVDAALNDLVPDGGEEE | 108 |
| RESULT 3 | | | |
| US-08-529-055-69 | | | |
| ; Sequence 69, Application US/08529055 | | | |
| ; Patent No. 6592876 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Briles, David E. | | | |
| ; APPLICANT: McDaniel, Larry S. | | | |
| ; APPLICANT: Swiatlo, Edwin | | | |
| ; APPLICANT: Iother, Janet | | | |
| ; APPLICANT: Brooks-Walter, Alexis | | | |
| ; TITLE OF INVENTION: Pneumococcal Genes, Portions | | | |
| ; TITLE OF INVENTION: Thereof, Expression Products | | | |
| ; TITLE OF INVENTION: Therefrom, and Uses of Such Genes, | | | |
| ; TITLE OF INVENTION: Portions and Products | | | |
| ; NUMBER OF SEQUENCES: 73 | | | |
| ; CORRESPONDENCE ADDRESS: | | | |
| ; ADDRESSEE: Curtis, Morris & Safford, P.C. | | | |
| ; STREET: 530 Fifth Avenue | | | |
| ; CITY: New York | | | |
| ; STATE: NY | | | |
| ; COUNTRY: USA | | | |
| ; ZIP: 10036 | | | |
| ; COMPUTER READABLE FORM: | | | |
| ; MEDIUM TYPE: Floppy disk | | | |
| ; COMPUTER: IBM PC compatible | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.30 | | | |
| ; CURRENT APPLICATION DATA: | | | |
| ; APPLICATION NUMBER: US/08/529,055 | | | |
| ; FILING DATE: 15-SEP-1995 | | | |
| ; CLASSIFICATION: 435 | | | |
| ; ATTORNEY/AGENT INFORMATION: | | | |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 20.7935 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-26
Perfect score: 540
Sequence: 1 LEKAEAELENLLTLDPGGK.....TPQEVDAALNDIVDPGGSEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 538 | 99.6 | 108 | 4 | US-09-147-875A-26 |
| 3 | 512 | 94.8 | 185 | 4 | US-08-529-055-69 |
| 4 | 512 | 94.8 | 8991 | 4 | US-08-714-741-32 |
| 5 | 461 | 85.4 | 108 | 2 | US-08-710-749-26 |
| 6 | 461 | 85.4 | 108 | 4 | US-09-147-875A-23 |
| 7 | 461 | 85.4 | 211 | 4 | US-08-529-055-67 |
| 8 | 454 | 84.1 | 108 | 4 | US-09-147-875A-24 |
| 9 | 447 | 82.8 | 108 | 2 | US-08-710-749-22 |
| 10 | 447 | 82.8 | 108 | 2 | US-08-710-749-23 |
| 11 | 447 | 82.8 | 212 | 4 | US-08-529-055-68 |
| 12 | 439 | 81.3 | 106 | 4 | US-09-147-875A-22 |
| 13 | 414 | 76.7 | 108 | 2 | US-08-710-749-24 |
| 14 | 414 | 76.7 | 108 | 4 | US-09-147-875A-25 |
| 15 | 414 | 76.7 | 232 | 4 | US-08-529-055-70 |
| 16 | 414 | 76.7 | 458 | 4 | US-08-529-055-73 |
| 17 | 274 | 50.7 | 104 | 2 | US-08-710-749-20 |
| 18 | 270 | 50.0 | 213 | 4 | US-08-529-055-47 |
| 19 | 266 | 49.3 | 104 | 4 | US-09-147-875A-21 |
| 20 | 263 | 48.7 | 104 | 2 | US-08-710-749-19 |
| 21 | 263 | 48.7 | 104 | 4 | US-09-147-875A-20 |
| 22 | 257 | 47.6 | 641 | 3 | US-08-961-083-160 |
| 23 | 257 | 47.6 | 641 | 4 | US-09-536-784-160 |
| 24 | 254 | 47.0 | 197 | 4 | US-08-529-055-44 |
| 25 | 244 | 45.2 | 233 | 4 | US-08-529-055-52 |
| 26 | 243 | 45.0 | 102 | 2 | US-08-710-749-21 |
| 27 | 243 | 45.0 | 102 | 4 | US-09-147-875A-18 |

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| 28 | 231.5 | 42.9 | 119 | 2 | US-08-710-749-27 | Sequence 27, Appl |
| 29 | 231.5 | 42.9 | 119 | 4 | US-09-147-875A-27 | Sequence 27, Appl |
| 30 | 231.5 | 42.9 | 215 | 4 | US-08-529-055-43 | Sequence 43, Appl |
| 31 | 186 | 34.4 | 80 | 2 | US-08-710-749-18 | Sequence 18, Appl |
| 32 | 186 | 34.4 | 80 | 4 | US-09-147-875A-19 | Sequence 19, Appl |
| 33 | 167 | 30.9 | 204 | 4 | US-08-529-055-51 | Sequence 51, Appl |
| 34 | 167 | 30.9 | 288 | 3 | US-08-312-949-4 | Sequence 4, Appl |
| 35 | 167 | 30.9 | 288 | 3 | US-08-446-201-4 | Sequence 4, Appl |
| 36 | 167 | 30.9 | 289 | 1 | US-08-072-070-4 | Sequence 4, Appl |
| 37 | 167 | 30.9 | 289 | 1 | US-08-469-434-4 | Sequence 4, Appl |
| 38 | 167 | 30.9 | 289 | 1 | US-08-214-222-4 | Sequence 4, Appl |
| 39 | 167 | 30.9 | 289 | 2 | US-08-467-852A-5 | Sequence 5, Appl |
| 40 | 167 | 30.9 | 289 | 2 | US-08-468-718-4 | Sequence 4, Appl |
| 41 | 167 | 30.9 | 289 | 1 | US-08-247-491A-5 | Sequence 5, Appl |
| 42 | 167 | 30.9 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |
| 43 | 167 | 30.9 | 619 | 1 | US-08-214-164-2 | Sequence 2, Appl |
| 44 | 167 | 30.9 | 619 | 2 | US-08-467-852A-3 | Sequence 3, Appl |
| 45 | 167 | 30.9 | 619 | 2 | US-08-246-636-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-710-749-25
; Sequence 25, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/POCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-25

Query Match 99.6%; Score 538; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEKAEAELENLLTLDPGGKTQDELDGAAAEALNKKVKEALPNPVXEELEELSPEDNLK 60
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DB 1 LEKAEAELENLLTLDPGGKTQDELDGAAAEALNKKVKEALPNPVXEELEELSPEDNLK 60
|||||

| | | |
|----|--|---|
| Db | : : : : | 76 LAKQTELEKLLDNLDPQKQDELDKEAAEAELDKKADLQNKVADLEKEISNLEILIG 135 |
| Qy | : : : : : : : : | 54 --PPDNLKDAETNHVEDYIKEGLEEATKQAELEETPOEVDAAALNDLVDPDGSEE 108 |
| Db | : : : : : : : : | 136 GADPEDD-----TAAQNKLATKKALEKTQKELDAAALNELGPDGDDEE 179 |

Search completed: November 17, 2005, 20:37:54
Job time : 65.0187 secs

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OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254255; AAF68090.1; -.
FT NON_TER 1
FT NON_TER 257
SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 57.5%; Score 310.5; DB 2; Length 257;
Best Local Similarity 58.0%; Pred. No. 4.1e-14;
Matches 69; Conservative 14; Mismatches 25; Indels 11; Gaps 2;

QY 1 LEKAEAELENLSTLDPGGKTQDELKGAEE-----AELNKKVEALPNPVXLELESPPE 56
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 51 LEKAEAELENLSTLDPGGKTQDELKGAEEADANIEALQNKVADLENKVAELEKVTQLQ 110
QY 57 DNLDKAETNHVEDYIKEGLEEAIAATKQAELEET-----POEYDAALNDLVPDGGEE 108
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 SLDKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAQAALDNLGPDGDEE 169

RESULT 10
QYLA6 PRELIMINARY; PRT; 461 AA.
ID Q9LAX6
AC Q9LAX6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6303;
RX MEDLINE=20448953; PubMed=10992499;
RA DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071820; AAF27715.1; -.
FT NON_TER 461
FT NON_TER 461
SQ SEQUENCE 461 AA; 51563 MW; 249435F65585BB92 CRC64;

Query Match 54.7%; Score 295.5; DB 2; Length 461;
Best Local Similarity 54.6%; Pred. No. 8.6e-13;
Matches 65; Conservative 16; Mismatches 27; Indels 11; Gaps 2;

QY 1 LEKAEAELENLSTLDPGGKTQDELKGAEE-----AELNKKVEALPNPVXLELESPPE 56
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 273 LEKAEAELENLSTLDPGGKTQDELKGAEEADANIEALQNKVADLENKVAELEKVTQLQ 332
QY 57 DNLDKAETNHVEDYIKEGLEEAIAATKQAELEET-----POEYDAALNDLVPDGGEE 108
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 333 SLDKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAQAALDNLGPDGDEE 391

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RESULT 11
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ID Q9LS95
AC Q9LS95;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254254; AAF68089.1; -.
FT NON_TER 1
FT NON_TER 256
FT NON_TER 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match 53.2%; Score 287.5; DB 2; Length 256;
Best Local Similarity 53.8%; Pred. No. 1.7e-12;
Matches 64; Conservative 16; Mismatches 28; Indels 11; Gaps 2;

QY 1 LEKAEAELENLSTLDPGGKTQDELKGAEE-----AELNKKVEALPNPVXLELESPPE 56
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 LEKAEAELENLSTLDPGGKTQDELKGAEEADANIEALQNKVADLENKVAELEKVTQLQ 111
QY 57 DNLDKAETNHVEDYIKEGLEEAIAATKQAELEET-----POEYDAALNDLVPDGGEE 108
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 SLDKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAQAALDNLGPDGDEE 170

RESULT 12
Q9KGS0 PRELIMINARY; PRT; 227 AA.
ID Q9KGS0
AC Q9KGS0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA protein (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RA Beall B.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288751; AAF91495.1; -.

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QY 1 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLK 60
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QY 61 DAETNHVEDYIKEGLEEAATKQAELEETPOEVDAAALNDLVPDGGEE 107
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Db 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 107

RESULT 6
Q8GNS7 PRELIMINARY; PRT; 213 AA.
AC Q8GNS7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=128;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490268; AAN37736.1; -.
FT NON_TER 1
FT NON_TER 213
FT NON_TER 213
SQ SEQUENCE 213 AA; 23490 MW; 23B4428409526EAB CRC64;

Query Match 77.4%; Score 418; DB 2; Length 213;
Best Local Similarity 81.5%; Pred. No. 1.1e-21;
Matches 88; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLK 60
|||||
Db 26 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALQNVAAEELEELSKLEDNLK 85
|||||
QY 61 DAETNHVEDYIKEGLEEAATKQAELEETPOEVDAAALNDLVPDGGEE 108
|||||
Db 86 VAETNNVEDYIKKGLAEATKQAELEKTQKALDTALNELGPDGDEE 133
|||||

RESULT 7
Q34097 PRELIMINARY; PRT; 653 AA.
AC Q34097;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PspA.
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF5668;
RX MEDLINE=98427139; PubMed=9746574;
RA McDaniel L.S., McDaniel D.O., Hollingshead S.K., Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
RT to the previously identified PspA sequence from strain Rxi and ability
RT of PspA from EF5668 to elicit protection against pneumococci of
RT different capsular types.";
RL Infect. Immun. 66:4748-4754(1998).
```

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DR EMBL; U89711; AAC62252.1; -.
DR HSP; P06653; IHCK.
DR InterPro; IPR002479; CW binding.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR009053; Prefoldin.
DR Pfam; PF01473; CW_binding_1; 9.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

Query Match 76.7%; Score 414; DB 2; Length 653;
Best Local Similarity 79.6%; Pred. No. 6.9e-21;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALPNPVXEELEELSPEDNLK 60
|||||
Db 276 LEDAELEKVLATLDPGKQTQDELKGAAEALNKKVEALQNVAAEELEELSKLEDNLK 335
|||||
QY 61 DAETNHVEDYIKEGLEEAATKQAELEETPOEVDAAALNDLVPDGGEE 108
|||||
Db 336 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 383
|||||

RESULT 8
Q8GNT0 PRELIMINARY; PRT; 211 AA.
AC Q8GNT0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP95;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490265; AAN37733.1; -.
FT NON_TER 1
FT NON_TER 211
FT NON_TER 211
SQ SEQUENCE 211 AA; 23207 MW; 096BFBE0B8CD6483 CRC64;

Query Match 57.5%; Score 310.5; DB 2; Length 211;
Best Local Similarity 58.0%; Pred. No. 3.4e-14;
Matches 69; Conservative 14; Mismatches 25; Indels 11; Gaps 2;

QY 1 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALPNPVXEELEELSPPE 56
|||||
Db 5 LEKAAELENLLSTLDPGKQTQDELKGAAEALNKKVEALQNVAAEELEELSKLEDNLK 64
|||||
QY 57 DNLKDAETNHVEDYIKEGLEEAATKQAELEET-----POEVDAAALNDLVPDGGEE 108
|||||
Db 65 SDLKDAEENNVYKGLAEATKKALEKTQKALDTALNELGPDGDEE 123
|||||

RESULT 9
Q9L594 PRELIMINARY; PRT; 257 AA.
AC Q9L594;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG7817;
RX MEDLINE=20448953; PubMed=10992499;
DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071826; AAF27719.1; -.
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 479
SQ SEQUENCE 479 AA; 53257 MW; B9C0D2CA15DE3654 CRC64;

Query Match 82.4%; Score 445; DB 2; Length 479;
Best Local Similarity 86.1%; Pred. No. 3.4e-23;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALPNPVXEEELSPEDNLK 60
Db 295 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALQNVXAELEELSKLEDNLK 354

Qy 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 355 DAETHNVEDYIKGLEEAIATKQAELETKQKELDAALNELGPDGDEE 402

RESULT 3
Q9LAX5 PRELIMINARY; PRT; 481 AA.
ID Q9LAX5;
AC Q9LAX5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG11703;
RX MEDLINE=20448953; PubMed=10992499;
DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071821; AAF27716.1; -.
DR HSP; P58301; 1L8D.
FT NON_TER 481
SQ SEQUENCE 481 AA; 53500 MW; EA3C66445EFCE2B CRC64;

Query Match 82.4%; Score 445; DB 2; Length 481;
Best Local Similarity 86.1%; Pred. No. 3.5e-23;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALPNPVXEEELSPEDNLK 60
Db 295 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALQNVXAELEELSKLEDNLK 354

Qy 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 355 DAETHNVEDYIKGLEEAIATKQAELETKQKELDAALNELGPDGDEE 402

RESULT 4
Q9L5B4 PRELIMINARY; PRT; 246 AA.
ID Q9L5B4;
AC Q9L5B4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP198;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
pneumococcal strains in the United States and of internationally
disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP198;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253408; AAF67356.1; -.
DR HSP; P05412; 1JNM.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26972 MW; 2190BED1460D26D9 CRC64;

Query Match 81.7%; Score 441; DB 2; Length 246;
Best Local Similarity 85.2%; Pred. No. 3.2e-23;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALPNPVXEEELSPEDNLK 60
Db 52 LEKAAELENLSTLDPGKQTQDELKGAAEALNKKEALQNVXAELEELSKLEDNLK 111

Qy 61 DAETHNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108
Db 112 DAETHNVEDYIKGLEEAIATKQAELETKQKELDAALNELGPDGDEE 159

RESULT 5
Q8KQK2 PRELIMINARY; PRT; 107 AA.
ID Q8KQK2;
AC Q8KQK2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Pneumococcal surface protein A (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255/00;
RX MEDLINE=22170754; PubMed=12183557;
DOI=10.1128/IAI.70.9.5086-5090.2002;
RA Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C.,
RA Dias W.O., Leite L.C.C.;
RT "Analysis of serum cross-reactivity and cross-protection elicited by
immunization with DNA vaccines against Streptococcus pneumoniae
expressing PspA fragments from different clades.";
RL Infect. Immun. 70:5086-5090(2002).
DR EMBL; AY082390; AAF92495.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

Query Match 80.7%; Score 436; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 2.9e-23;
Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
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| Result No. | Score | Query % | | DB | ID | Description |
|------------|-------|---------|--------|----|---------|---------------------|
| | | Match | Length | | | |
| 1 | 463 | 85.7 | 480 | 2 | Q9LAX3 | Q9Lax3 streptococc |
| 2 | 445 | 82.4 | 479 | 2 | Q9LAX2 | Q9Lax2 streptococc |
| 3 | 445 | 82.4 | 481 | 2 | Q9LAX5 | Q9Lax5 streptococc |
| 4 | 441 | 81.7 | 246 | 2 | Q9L5B4 | Q9L5b4 streptococc |
| 5 | 436 | 80.7 | 107 | 2 | Q8KQK2 | Q8Kqk2 streptococc |
| 6 | 418 | 77.4 | 213 | 2 | Q8GNS7 | Q8gns7 streptococc |
| 7 | 414 | 76.7 | 653 | 2 | Q34097 | Q34097 streptococc |
| 8 | 310.5 | 57.5 | 211 | 2 | Q8GN70 | Q8gnt0 streptococc |
| 9 | 310.5 | 57.5 | 257 | 2 | Q9L594 | Q9L594 streptococc |
| 10 | 295.5 | 54.7 | 461 | 2 | Q9LAX6 | Q9Lax6 streptococc |
| 11 | 287.5 | 53.2 | 256 | 2 | Q9L595 | Q9L595 streptococc |
| 12 | 284.5 | 52.7 | 227 | 2 | Q9LKG80 | Q9Lkgs0 streptococc |
| 13 | 275 | 50.9 | 242 | 2 | Q9L562 | Q9L562 streptococc |
| 14 | 263 | 48.7 | 222 | 2 | Q9L584 | Q9L584 streptococc |
| 15 | 261 | 48.3 | 231 | 2 | Q9L579 | Q9L579 streptococc |
| 16 | 261 | 48.3 | 241 | 2 | Q9L580 | Q9L580 streptococc |
| 17 | 258 | 47.8 | 228 | 2 | Q9L5B8 | Q9L5b8 streptococc |
| 18 | 258 | 47.8 | 235 | 2 | Q9L582 | Q9L582 streptococc |
| 19 | 258 | 47.8 | 249 | 2 | Q9L5D4 | Q9L5d4 streptococc |
| 20 | 258 | 47.8 | 252 | 2 | Q9L583 | Q9L583 streptococc |
| 21 | 258 | 47.8 | 360 | 2 | Q8KQK3 | Q8Kqk3 streptococc |
| 22 | 258 | 47.8 | 429 | 2 | Q9LAX7 | Q9Lax7 streptococc |
| 23 | 258 | 47.8 | 526 | 2 | Q9LAX9 | Q9Lax9 streptococc |
| 24 | 258 | 47.8 | 608 | 2 | Q8VQ55 | Q8vg55 streptococc |
| 25 | 258 | 47.8 | 744 | 2 | Q97T39 | Q97L39 streptococc |
| 26 | 257 | 47.6 | 249 | 2 | Q9L5B7 | Q9L5b7 streptococc |
| 27 | 257 | 47.6 | 502 | 2 | Q9LAX8 | Q9Lax8 streptococc |
| 28 | 256 | 47.4 | 249 | 2 | Q9L585 | Q9L585 streptococc |
| 29 | 256 | 47.4 | 256 | 2 | Q9L590 | Q9L590 streptococc |
| 30 | 249 | 46.1 | 209 | 2 | Q9L593 | Q9L593 streptococc |
| 31 | 178 | 33.0 | 117 | 2 | Q9L1AY3 | Q9L1ay3 streptococc |

Query Match 18.5%; Score 100; DB 2; Length 1937;
 Best Local Similarity 31.5%; Pred. No. 16;
 Matches 29; Conservative 15; Mismatches 34; Indels 14; Gaps 2;

QY 1 LEKAELENLSTLDPGGKTQDELDKGAEEAELNKKVEALPNPVXLEEEELSPEDNLK 60
 Db 1083 LEKKEFEISNLISKIE-----DEQAVEIQLOKKIKELQARIEELGEEIEAERASRA 1133
 QY 61 DAETNHVE-----DYIKEGLEEAIAIKQAELE 87
 Db 1134 KAEKQSDLSRELEISERLEAEAGGATSAQVE 1165

RESULT 15
 S21880
 dnaK-type molecular chaperone blp5 precursor - common tobacco
 N:Alternate names: luminal binding protein blp5
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C:Accession: S21880; JQ1361
 R:Denecke, J.; Goldman, M.H.; Demolder, J.; Seurinck, J.; Botterman, J.
 submitted to the EMBL Data Library, June 1991
 A:Description: The luminal binding protein (BiP) is encoded by a multigene family in tobacco
 A:Reference number: S21877
 A:Accession: S21880
 A:Molecule type: mRNA
 A:Residues: 1-668 <DEN>
 A:Cross-references: UNIPROT:Q03685; EMBL:X60058; NID:g19812; PIDN:CAA42660.1; PID:g19813
 R:Denecke, J.; Goldman, M.H.S.; Demolder, J.; Seurinck, J.; Botterman, J.
 Plant Cell 3, 1025-1035, 1991
 A:Title: The tobacco luminal binding protein is encoded by a multigene family.
 A:Reference number: JQ1360; MUID:92361242; PMID:1822990
 A:Accession: JQ1361
 A:Molecule type: mRNA
 A:Residues: 1-653,'G', 655-668 <DEW>
 A:Note: translation of the nucleotide sequence is not complete
 C:Genetics:
 A:Gene: blp5
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein complex
 A:Superfamily: heat shock protein 70
 C:Keywords: ATP; endoplasmic reticulum; molecular chaperone
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:665-668/Region: endoplasmic reticulum retention signal

Query Match 18.4%; Score 99.5; DB 2; Length 668;
 Best Local Similarity 26.9%; Pred. No. 5.2;
 Matches 36; Conservative 23; Mismatches 48; Indels 27; Gaps 5;

QY 2 EKAEELENLSTLDPGGKTQDELDKGAEE-----AELNKKVE-----ALPNPVXLEEE 50
 Db 524 DKASGKSEKITITNKGRLSQEIERVMYKAEFEAEEDKKVKERIDARNSLETYYNNRN 583
 QY 51 ELSPPE---DNLKDAETHNVEDYIKEGLEEAIAIKQAELE---ETPQVEDAALNDLV--- 101
 Db 584 QINDKDKLADKLESDKKEIKETATKEALEWLDNQSAEKDYDEKLEVEAVCNPIITAV 643
 QY 102 -----PDGEEEE 108
 Db 644 YORSGAGPGGASEE 657

Search completed: November 17, 2005, 20:39:54
 Job time : 15.1144 secs

QY 2 EKAE-----AELENLLSTLDPGKTODELDKGAAEALNKVKVTEALNPVPXVEELBEEL 52
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 1491 QKAELRVNKKQFRTEMEDLMSSDDYGVKS VHELEK--AKRALQQOVBEMTKTGLEEDEL 1548

QY 53 SPPEDNLKOAEETHNVE-----DYIKGLEGEEAIATKQAELLETPOEVDAALND 99
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 1549 QATEDAKLRILEVNQQAWKAQFDRDLLGRDQENBKRQLRIQRVREMEVEUDED 1600

RESULT 14
I38055
N;Contains heavy chain, perinatal skeletal muscle - human
C;Species: myosin Appase (EC 3.6.4.1)
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
C;Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R;Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Sted
Eur. J. Biochem. 230, 1001-1006, 1995
A;Title: Characterization of a human perinatal myosin heavy-chain transcript.
A;Reference number: I38055; MUID:95324556; PMID:7601129
A;Accession: I38055
A>Status: preliminary; translated from GB/EMBL/DDBBJ
A;Molecule type: mRNA
A;Residues: 1-1937 <RES>
A;Cross-references: UNIPROT:P13535; EMBL:Z38133; NID:g558668; PIDN:CAA86293.1;
R;Karsch-Mizrachi, I.; Feghalli, R.; Shows, T.B.; Leinwand, L.A.
Gene 89, 289-294, 1990
A;Title: Generation of a full-length human perinatal myosin heavy-chain encoding
A;Reference number: JH0154; MUID:90323631; PMID:237371
A;Accession: JH0154
A;Molecule type: mRNA
A;Residues: 1-14, 'A', 16-859 <VAR>
A;Cross-references: GB:Y00821
A;Experimental source: skeletal muscle
R;Bober, E.
submitted to the EMBL Data Library, January 1989
A;Reference number: S12458
A;Accession: S12459
A;Molecule type: mRNA
A;Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937
A;Cross-references: EMBL:X51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A;Experimental source: clone gTMHC-F
R;Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, I.
Eur. J. Biochem. 189, 55-65, 1990
A;Title: Identification of three developmentally controlled isoforms of human m
A;Reference number: S09331; MUID:90235862; PMID:1691980
A;Accession: S09332
A;Molecule type: mRNA
A;Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897
-1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X'
A;Cross-references: EMBL:X51592
R;Feghalli, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A;Title: Molecular genetic characterization of a developmentally regulated human
A;Reference number: A30220; MUID:89234168; PMID:2715179
A;Accession: A30220
A>Status: preliminary
A;Molecule type: mRNA
A;Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH',
A;Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
C;Genetics:
A;Gene: GDB:MVH8
A;Cross-references: GDB:125267; OMIM:160741
A;Map position: 17pter-17p12
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolyase
P;91-/69/Domain: myosin motor domain homology <MMOT>
F;181-188/Region: nucleotide-binding motif A (P-loop)
F;551-588/Region: actin binding #status predicted
F;558-680/Region: actin binding #status predicted
F;842-1283/Region: S2 #status predicted
F;698,708/Active site: Cys #status predicted

[illegible]

C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: D71453
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hainaka, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71453
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-279 <KAW>
A:Cross-references: UNIPROT:058021; GB:AP000001; NID:g3236128; PIDN:BAA29355.1; PID:g325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0283

Query Match 19.8%; Score 107; DB 2; Length 279;
Best Local Similarity 31.0%; Pred. No. 0.55;
Matches 36; Conservative 20; Mismatches 48; Indels 12; Gaps 3;

QY 1 LEKAAELENLSTLDPGGKTQDELKGAABAEALN-----KKVEALPNPVXEELEEL 52
DB 164 LEKAAELENLSTLDPGGKTQDELKGAABAEALN-----KKVEALPNPVXEELEEL 52
QY 53 SPPELNKDAETHNVE-DYIKGLEEAATKQAELEETPQEVDA---ALNDLVDPG 104
DB 224 REIEGRKDYEEKIRELEKEEKGLEEKINVLNRIENLKNGRSAKEALRLEEG 279

RESULT 6
A59282
nonmuscle myosin II heavy chain A - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59282
R:Bhati.Dev, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
Mech. Dev. 78, 33-36, 1998
A:Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e
A:Reference number: A59282; MUID:99077683; PMID:9858676
A:Accession: A59282
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1964 <BHA>
A:Cross-references: UNIPROT:093522; GB:AF055895; NID:g3660671; PIDN:AAC83556.1; PID:g366
A:Experimental source: cell line XTC
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:84-764/Domain: myosin motor domain homology <NMO>

Query Match 19.4%; Score 104.5; DB 2; Length 1964;
Best Local Similarity 28.6%; Pred. No. 7.5;
Matches 30; Conservative 24; Mismatches 40; Indels 11; Gaps 3;

QY 2 EKAEEALENLSTLDPGGKTQDELKGAABAEALNKKVEALPNPVXEELEELSPPED 57
DB 1500 KQLRTMEDLVSKDDVGVKSHVELEK--SKRALEQQAEMTKQLELEDELQATEDAKLR 1557

QY 58 ---NLKDAETHNVEDYIKGLEEAATKQAELEETPQEVDAALND 99
DB 1558 LEVNLQAMKAQFERDL--QGRDEQSEDKKQLVQVKMEAELE 1600

RESULT 7
A47297
myosin heavy chain form B, nonmuscle - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47297; A55441
R:Bhati.Dev, N.; Adelstein, R.S.; Dawid, I.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993
A:Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmuscl
A:Reference number: A47297; MUID:93219383; PMID:8464900

A:Accession: A47297
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1992 <BHA>
A:Cross-references: UNIPROT:004834; GB:I09740; NID:g214623; PIDN:AAA49915.1; PID:g21462
A:Experimental source: XTC cells
A:Note: sequence extracted from NCBI backbone (NCBIP:128722)
R:Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.
J. Biol. Chem. 270, 1395-1401, 1995
A:Title: A Xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34
A:Reference number: A55441; MUID:95138137; PMID:7836406
A:Accession: A55441
A:Status: preliminary
A:Molecule type: protein
A:Residues: 198-232 <KEL>
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:88-787/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 19.4%; Score 104.5; DB 2; Length 1992;
Best Local Similarity 30.5%; Pred. No. 7.6;
Matches 32; Conservative 22; Mismatches 40; Indels 11; Gaps 3;

QY 2 EKAEEALENLSTLDPGGKTQDELKGAABAEALNKKVEALPNPVXEELEELSPPEDNLKD 61
DB 1522 KQLRAEMEDLVSKDDVGVKSHVELEK--SKRALDQQVEEMRTQLELEDELQGTEDAKLR 1579

QY 62 AETHNVEDYIKGLEEAATKQAELEETP-----QEVDAALND 99
DB 1580 LEVN--MQAMKAQFERDLQTRDQNEKKRALVKQVRELEAELE 1622

RESULT 8
Ti4156
kinesin-related protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4156
R:Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
Cell 91, 357-366, 1997
A:Title: KENP-E is a plus end-directed kinetochore motor required for metaphase chromosom
A:Reference number: Z17893; MUID:98028574; PMID:9363944
A:Accession: Ti4156
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2954 <WOO>
A:Cross-references: UNIPROT:042263; EMBL:AF027728; NID:g2586070; PID:g2586071; PIDN:AAC6
C:Genetics:
A:Gene: XCENP-E
C:Superfamily: centromere protein E; kinesin motor domain homology

Query Match 19.0%; Score 102.5; DB 2; Length 2954;
Best Local Similarity 28.1%; Pred. No. 17;
Matches 32; Conservative 18; Mismatches 43; Indels 21; Gaps 3;

QY 2 EKAEEALENLSTLDPG---GKTQDELKGAABAEALNKKVEALPNPVXEELEELSPPED 57
DB 1952 EQALNTEHLRETLTKSLKDLALGKMEQERDEA-----NKVIALTEKVSLEEQINENVT 2005

QY 58 NLKDAETHNVEDYIK-----EGLEEAATKQAELEETPOEVDAALNDL 100
DB 2006 TLKEGEKEKTFYLQRPQKQSSSQMSELRLSKTKDLQLEAAEKISEATNEI 2059

RESULT 9
Ti4261
dnak-type molecular chaperone - common sunflower (fragment)
N:Alternate names: HSP70-related protein
C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4261
R:Courbou, I.; Badaoui, S.; Gentzbittel, L.; Mouzeyar, S.; Nicolas, P.

A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:AE007317; PIDN:AAK98925.1; PID:gl
C;Genetics:
A;Gene: pspA

Query Match 30.9%; Score 167; DB 2; Length 619;
Best Local Similarity 39.6%; Pred. No. 5.3e-05;
Matches 44; Conservative 20; Mismatches 29; Indels 18; Gaps 3;

Qy 6 AELENLLSTLDPGGKTQDELK-----GAAPAEALNKVKEALPNPVXLE 49
Db 210 AELENQVHRLEQELKEIDSESEDYAKGFRAPLQSKLDAKKALUS-KLEELSDKIDELD 268

Qy 50 EELSPEDNLKDA-ETNHVEDYIKGLEEAATKQAELEETPOEVDAALND 99
Db 269 AEIAKLEQLKAAEENNNVVDYFKGLEKTIAAKKAELEKTEADLKAVNE 319

RESULT 3
A1971
surface protein pspA precursor - Streptococcus pneumoniae
N;Alternate names: pneumococcal surface protein A
C;Species: Streptococcus pneumoniae
C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A41971; A60282; A33134
R;Yother, J.; Briles, D.E.
J. Bacteriol. 174, 601-609, 1992
A;Title: Structural properties and evolutionary relationships of PspA, a surface protein
A;Reference number: A41971; MUID:92105030; PMID:1729249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-619 <YOT>
A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:M74122; NID:G153840; PIDN:AAA2701
A;Note: sequence extracted from NCBI backbone (NCBIN:75635, NCBIIP:75636)
R;Talkington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.E.
Infect. Immun. 59, 1285-1289, 1991
A;Title: A 43-kilodalton pneumococcal surface protein, PspA: isolation, protective ability
A;Reference number: A60282; MUID:91169598; PMID:2004810
A;Accession: A60282
A;Molecule type: protein
A;Residues: 32-76 <TAL>
A;Experimental source: strain JY2008
C;Genetics:
A;Gene: pspA
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-619/Product: surface protein pspA #status predicted <MAT>
F;411-430/Domain: cpl repeat homology <CP01>
F;431-450/Domain: cpl repeat homology <CP02>
F;451-470/Domain: cpl repeat homology <CP03>
F;471-490/Domain: cpl repeat homology <CP04>
F;491-510/Domain: cpl repeat homology <CP05>
F;511-530/Domain: cpl repeat homology <CP06>
F;531-550/Domain: cpl repeat homology <CP07>
F;551-570/Domain: cpl repeat homology <CP08>
F;571-591/Domain: cpl repeat homology <CP09>
F;592-611/Domain: cpl repeat homology <CP10>

Query Match 30.9%; Score 167; DB 2; Length 619;
Best Local Similarity 39.6%; Pred. No. 5.3e-05;
Matches 44; Conservative 20; Mismatches 29; Indels 18; Gaps 3;

Qy 6 AELENLLSTLDPGGKTQDELK-----GAAPAEALNKVKEALPNPVXLE 49
Db 210 AELENQVHRLEQELKEIDSESEDYAKGFRAPLQSKLDAKKALUS-KLEELSDKIDELD 268

Qy 50 EELSPEDNLKDA-ETNHVEDYIKGLEEAATKQAELEETPOEVDAALND 99
Db 269 AEIAKLEQLKAAEENNNVVDYFKGLEKTIAAKKAELEKTEADLKAVNE 319

RESULT 4
A61231
myosin heavy chain nonmuscle form A - human

N;Alternate names: cellular myosin heavy chain; myosin type 9; NMHC-A
N;Contains: myosin ATPase (SC 3.6.4.1)
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61231; A34876; I52562; I61692
R;Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, C.
Circ. Res. 69, 530-539, 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on different chromosomes
A;Reference number: A61231; MUID:91316803; PMID:1860190
A;Accession: A61231
A;Molecule type: mRNA
A;Residues: 1-715 <SIM>
A;Cross-references: UNIPROT:P35579; UNIPROT:Q9UMJ0; GB:M69180; NID:G189029; PIDN:AAA6176
R;Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990
A;Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alternative splicing
A;Reference number: A34876; MUID:90138958; PMID:1967836
A;Accession: A34876
A;Molecule type: mRNA
A;Residues: 715-1961 <SAE>
A;Cross-references: GB:M31013; NID:G189035; PIDN:AAA36349.1; PID:G189036
R;Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.; Blood 78, 1826-1833, 1991
A;Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, cDNA sequencing, and expression in transgenic mice
A;Reference number: I52562; MUID:92003925; PMID:1912569
A;Accession: I52562
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-52 'EAT', 56-659, 'T', 661-868, 'T', 870-930 'C', 932-1239, 'KG', 1242-1337 <RES>
A;Cross-references: GB:M81105; NID:G188988; PIDN:AAAS988.1; PID:G553596
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin genes in Dictyostelium
A;Reference number: A55758; MUID:94294418; PMID:8022818
A;Accession: I61692
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 182-218 <BEM>
A;Cross-references: GB:L29141; NID:G457249; PIDN:AAA20904.1; PID:G531134
C;Genetics:
A;Gene: GDB:MVH9
A;Cross-references: GDB:L20216; OMIM:160775
A;Map position: 22q12.3-22q13.1
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide binding site
F;84-764/Domain: myosin motor domain homology <NMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;552-565/Region: actin binding #status predicted
F;626-640/Region: actin binding #status predicted
F;837-1938/Domain: coiled coil #status predicted <COI>
F;837-1277/Domain: S2 #status predicted <DS2>
F;1278-1961/Domain: light meromyosin #status predicted <LMW>
F;1939-1961/Domain: carboxyl-terminal <CRT>
F;125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;694,704/Active site: Cys #status predicted

Query Match 20.4%; Score 110; DB 1; Length 1961;
Best Local Similarity 29.8%; Pred. No. 2.9;
Matches 34; Conservative 23; Mismatches 37; Indels 20; Gaps 4;

Qy 2 EKAF-----AELENLLSTLDPGGKTQDELKGAAPAEALNKVKEALPNPVXLEEL 52
Db 1492 QKAELRLNKQFRTEMDLMSKDDVGVKSVELEK--SKRALEQQVEEMKTLQLEDEL 1549

Qy 53 SPPE-----NLKDAETHVEDYIKGLEEAATKQAELEETPOEVDAALND 99
Db 1550 QATEDAKRLLEVNLAQMAKQAFERDL--QGRDEOSEKKQLVROVREMEAELE 1601

RESULT 5
D71453
hypothetical protein PH0283 - Pyrococcus horikoshii


```

XX AAW14590;
AC
XX 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Ef5668.
XX
PN WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, Medaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
DR WPI; 1997-202002/18.
XX
PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
PS Example 6; Fig 13; 296pp; English.
XX
CC This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Ef5668 (see
CC also AAW14592). Comparison of the N-terminal and central regions
CC (AAW14533-57 and AAW14562-91) of PspA from different pneumococcal strains
CC can be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 233 AA;

Query Match 74.7%; Score 403.5; DB 2; Length 233;
Best Local Similarity 78.9%; Pred. No. 2.2e-30;
Matches 86; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 LEKAAELENLSTLDP-GGKTODELDKAAEALNKKVEALPNPVXLEBELSPEDNL 59
DB 51 LEDAELEKVLATLDPEGKTQDDELDRKAAEALNEKVEALQNVAELEBELSKLEDNL 110
QY 60 KDAETNHVEDYIKEGLEEAIAIKQAELKETPOEVDAALNDLVPDGGEEE 108
DB 111 KDAETNHVEDYIKEGLEEAIAIKQAELKETQKELDAALNELGPDGDEEE 159

Search completed: November 17, 2005, 20:19:43
Job time : 76.7468 secs

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Query Match          76.7%; Score 414; DB 7; Length 458;
Best Local Similarity 79.6%; Pred. No. 5e-31;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAEAELENLSTLDPGKGTODELDKGAAEAEINKKVEALPNPVXEEELSPEDNLK 60
DB 276 LEDAELELEKVLATLDPEGKTODELDKEAAEAEINKKVEALQNVAAELEEELSKLEDNLK 335

QY 61 DAETNNHVEDYIKEGLEEAIAATKQAELEETPOEVDAALNDLVPDGGEEE 108
DB 336 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 383

RESULT 13
ADK52495
ID ADK52495 standard; protein; 653 AA.
XX
AC ADK52495;
XX
XX 20-MAY-2004 (first entry)
XX
XX PspA molecule from the Rxl strain of Streptococcus pneumoniae.
XX
XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
KW Hodgkin's disease.
XX
XX Streptococcus pneumoniae.
XX
XX WO2004016231-A2.
XX
XX 26-FEB-2004.
XX
XX 17-FEB-2003; 2003WO-US008199.
XX
XX 15-MAR-2002; 2002US-0365351P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Briles DE;
XX
XX WPI; 2004-192068/18.
XX
XX Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX
XX Claim 17; SEQ ID NO 1; 41pp; English.
XX
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents PspA
CC molecule from the Rxl strain of Streptococcus pneumoniae.
XX
XX Sequence 653 AA;

Query Match          76.7%; Score 414; DB 8; Length 653;
Best Local Similarity 79.6%; Pred. No. 7.6e-31;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAEAELENLSTLDPGKGTODELDKGAAEAEINKKVEALPNPVXEEELSPEDNLK 60
DB 276 LEDAELELEKVLATLDPEGKTODELDKEAAEAEINKKVEALQNVAAELEEELSKLEDNLK 335

QY 61 DAETNNHVEDYIKEGLEEAIAATKQAELEETPOEVDAALNDLVPDGGEEE 108
DB 336 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 383
```

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RESULT 14
AD052080
ID AD052080 standard; protein; 653 AA.
XX
AC AD052080;
XX
XX 12-AUG-2004 (first entry)
XX
XX S. pneumoniae strain EF5688 PspA protein.
XX
XX Immunogenic composition; vaccine; Th2-type immune response;
KW pneumococcal surface protein A; PspA.
XX
XX Streptococcus pneumoniae.
XX
XX Key Location/Qualifiers
XX Peptide 1..31
XX /label= Signal_peptide
XX Protein 32..653
XX /note= "S. pneumoniae strain EF5688 mature PspA protein"
XX Domain 110..384
XX /note = PspA alpha-helical domain
XX
XX US2004101531-A1.
XX
XX 27-MAY-2004.
XX
XX 15-APR-2003; 2003US-00414532.
XX
XX 16-APR-2002; 2002US-0372710P.
XX
XX (CURT/) CURTISS R.
XX (KANG/) KANG H Y.
XX
XX Curtiss R, Kang HY;
XX
XX WPI; 2004-399655/37.
XX N-PSDB; AD052067.
XX
XX New vaccine comprising a live attenuated strain of pathogenic gram-
PT negative bacteria, useful in eliciting a Th2-type immune response in a
PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
PT or bacteria.
XX
XX Example 5; SEQ ID NO 26; 94pp; English.
XX
XX The invention relates to immunogenic compositions and vaccines comprising
CC a live attenuated strain of pathogenic gram negative bacteria that
CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
CC response in a vertebrate against pathogens, e.g., helminths, fungi,
CC viruses, protozoans or bacteria. The present sequence is Streptococcus
CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA). This
CC sequence is used in the exemplification of the invention.
XX
XX Sequence 653 AA;

Query Match          76.7%; Score 414; DB 8; Length 653;
Best Local Similarity 79.6%; Pred. No. 7.6e-31;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAEAELENLSTLDPGKGTODELDKGAAEAEINKKVEALPNPVXEEELSPEDNLK 60
DB 276 LEDAELELEKVLATLDPEGKTODELDKEAAEAEINKKVEALQNVAAELEEELSKLEDNLK 335

QY 61 DAETNNHVEDYIKEGLEEAIAATKQAELEETPOEVDAALNDLVPDGGEEE 108
DB 336 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 383

RESULT 15
AAW14590
ID AAW14590 standard; protein; 233 AA.
```


PS Claim 17; SEQ ID NO 2; 41pp; English.

XX The present invention relates to treating Streptococcus pneumoniae

CC infection in a subject lacking a functional spleen comprises

CC administering an antibody that recognizes pneumococcal surface protein A

CC (PspA) or its binding portion. The method is useful for treating or

CC preventing Streptococcus pneumoniae infection in a subject lacking a

CC functional spleen. The disease-associated injury is especially due to

CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell

CC anemia or Hodgkin's disease. The present sequence represents the alpha

CC helical region PspA molecule from the Rxi strain of Streptococcus

CC pneumoniae.

XX Sequence 369 AA;

SQ Query Match 76.7%; Score 414; DB 8; Length 369;

Best Local Similarity 79.6%; Pred. No. 3.8e-31;

Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAAELENLSTLDPGKTQDELKGAAEALNKKVEALPNVYEELEELSPEDNLK 60

DB 245 LEDAELEKVLATLDPEGKTQDELKGAAEALNKKVEALQNVAELEELSKLEDNLK 304

QY 61 DAETNNVEDYIKEGLEEAIAATKQAELETPQEVDAALNDLVPDGEDEE 108

DB 305 DAETNNVEDYIKEGLEEAIAATKQAELETKQKELDAALNELGPDGDEDEE 352

RESULT 11

AAW14592

ID AAW14592 standard; protein; 458 AA.

AC AAW14592;

XX 17-OCT-2003 (revised)

DT 27-OCT-1997 (first entry)

XX Streptococcus pneumoniae PspA surface protein.

DE PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;

KW bacteraemia; pneumonia.

XX Streptococcus pneumoniae; strain Ef5668.

OS WO9709994-A1.

PN Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

XX Hollingshead S, Tart R, Brooks-Walter A;

PD 20-MAR-1997.

XX 16-SEP-1996; 96WO-US014819.

PF 15-SEP-1995; 95US-00529055.

PR (UABR-) UAB RES FOUND.

XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

PI Hollingshead S, Tart R, Brooks-Walter A;

XX WPI; 1997-202002/18.

DR N-PSDB; AAT61724.

XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used

PT in vaccines for protecting animals against S.pneumoniae infection.

XX Disclosure; Fig 13; 296pp; English.

XX This sequence comprises the pneumococcal surface protein A (pspA) of

CC Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the

CC pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be

CC used in vaccines to protect animals against S. pneumoniae infection and

CC hence for the prevention of diseases such as otitis media, meningitis,

CC bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS

CC field)

SQ Sequence 458 AA;

Query Match 76.7%; Score 414; DB 2; Length 458;

Best Local Similarity 79.6%; Pred. No. 5e-31;

Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEKAAELENLSTLDPGKTQDELKGAAEALNKKVEALPNVYEELEELSPEDNLK 60

DB 276 LEDAELEKVLATLDPEGKTQDELKGAAEALNKKVEALQNVAELEELSKLEDNLK 335

QY 61 DAETNNVEDYIKEGLEEAIAATKQAELETPQEVDAALNDLVPDGEDEE 108

DB 336 DAETNNVEDYIKEGLEEAIAATKQAELETKQKELDAALNELGPDGDEDEE 383

RESULT 12

ABW02626

ID ABW02626 standard; protein; 458 AA.

XX ABW02626;

XX 12-FEB-2004 (first entry)

DE Ef5668 pneumococcal surface protein A (PspA).

XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;

KW immunological; gene therapy; immunostimulant.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 458

FT /note= "Encoded by GC"

XX US6592876-B1.

PN 15-JUL-2003.

PD 15-SEP-1995; 95US-00529055.

PF 20-APR-1993; 93US-00048896.

PR 06-JUN-1995; 95US-00465746.

XX (UABR-) UAB RES FOUND.

PA Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

PI WPI; 2003-862841/80.

DR N-PSDB; AAD64535.

XX Immunological composition for obtaining expression products used for

PT detecting the presence of Streptococcus pneumoniae or its strain,

PT comprises at least two different full length isolated gene encoding

PT pneumococcal surface protein A.

XX Example 6; SEQ ID NO 73; 121pp; English.

PS The present invention relates to an immunological composition comprising

CC at least 2 different full length isolated genes encoding pneumococcal

CC surface protein A (PspAs) from different groups based on restriction

CC fragment polymorphism analysis. The invention is useful for obtaining

CC expression products by recombinant techniques to detect, determine,

CC isolate or diagnose the presence of Streptococcus pneumoniae or its

CC strain. The expression product is useful for preparing antigenic,

CC immunological or vaccine compositions, for eliciting antibodies, an

CC immunological response (other than or additional to antibodies) or a

CC protective response (including antibody or other immunological response

CC by administering compositions to a host). The invention is also useful as

CC vaccines and in gene therapy. The present sequence is Ef5668 pneumococcal

CC surface protein A (PspA) used in the exemplification of the invention

XX Sequence 458 AA;

```
PN US6592876-B1.
XX
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.
XX
DR Immunological composition for obtaining expression products used for
XX PT detecting the presence of Streptococcus pneumoniae or its strain,
XX PT comprises at least two different full length isolated gene encoding
XX PT pneumococcal surface protein A.
XX
XX Example 6; SEQ ID NO 70; 121pp; English.
PS
PS The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspA) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is EF5688
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
XX Sequence 232 AA;
SQ
Query Match 76.7%; Score 414; DB 7; Length 232;
Best Local Similarity 79.6%; Pred. No. 2.2e-31;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 1 LEKAAELENLLSTDPGGKTQDELKGAAEALNKKVEALPNPVXEEELSPEDNLK 60
Db 51 LEDAELEKVLATLDPGGKTQDELKGAAEALNKKVEALQNVAAELEEELSKLEDNLK 110
QY 61 DAETNNVEDYIKGLEEAIATKQAELETPQEVDAALNDLVPDGGEE 108
Db 111 DAETNNVEDYIKGLEEAIATKQAELETKQKELDAALNELGPDGDEE 158
RESULT 9
AD052055
ID AD052055 standard; protein; 275 AA.
AC AD052055;
XX
XX 12-AUG-2004 (first entry)
DT
DE S. pneumoniae strain EF5688 PspA alpha helical domain.
XX
XX Immunogenic composition; vaccine; Th2-type immune response ;
KW pneumococcal surface protein A; PspA.
XX
XX Streptococcus pneumoniae.
OS
XX US2004101531-A1.
XX
XX 27-MAY-2004.
PD
XX 15-APR-2003; 2003US-00414532.
XX
XX
```

```
PR 16-APR-2002; 2002US-0372710P.
XX
XX (CURT/) CURTISS R.
XX (KANG/) KANG H Y.
XX
XX Curtiss R, Kang HY;
XX WPI; 2004-399655/37.
DR
XX
XX New vaccine comprising a live attenuated strain of pathogenic gram-
XX PT negative bacteria, useful in eliciting a Th2-type immune response in a
XX PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
XX PT or bacteria.
XX
XX Claim 17; SEQ ID NO 1; 94pp; English.
PS
XX The invention relates to immunogenic compositions and vaccines comprising
CC a live attenuated strain of pathogenic gram negative bacteria that
CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
CC response in a vertebrate against pathogens, e.g., helminths, fungi,
CC viruses, protozoans or bacteria. The present sequence is Streptococcus
CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
CC helical domain. This sequence is used in the invention.
XX
XX Sequence 275 AA;
SQ
Query Match 76.7%; Score 414; DB 8; Length 275;
Best Local Similarity 79.6%; Pred. No. 2.7e-31;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 1 LEKAAELENLLSTDPGGKTQDELKGAAEALNKKVEALPNPVXEEELSPEDNLK 60
Db 167 LEDAELEKVLATLDPGGKTQDELKGAAEALNKKVEALQNVAAELEEELSKLEDNLK 226
QY 61 DAETNNVEDYIKGLEEAIATKQAELETPQEVDAALNDLVPDGGEE 108
Db 227 DAETNNVEDYIKGLEEAIATKQAELETKQKELDAALNELGPDGDEE 274
RESULT 10
ADK52496
ID ADK52496 standard; protein; 369 AA.
XX
XX ADK52496;
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE alpha helical region PspA molecule from the Rx1 strain.
XX
XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
XX Hodgkin's disease.
XX
XX Streptococcus pneumoniae.
OS
XX WO2004016231-A2.
XX
XX 26-FEB-2004.
PD
XX
XX 17-FEB-2003; 2003WO-US008199.
XX
XX 15-MAR-2002; 2002US-0365351P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Briles DE;
XX
XX WPI; 2004-192068/18.
XX
XX Treating Streptococcus pneumoniae infection in a subject lacking a
XX functional spleen comprises administering an antibody that recognizes
XX PT pneumococcal surface protein A (PspA) or its binding portion.
XX
```

| | |
|-----------------------|--|
| AAW14588 | Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine; immunological; gene therapy; immunostimulant. |
| ID | AAW14588 standard; protein; 212 AA. |
| XX | |
| AC | AAW14588; |
| XX | |
| DT | 17-OCT-2003 (revised) |
| DT | 28-OCT-1997 (first entry) |
| XX | |
| DE | Streptococcus pneumoniae PspA central region. |
| XX | |
| KW | PspA; pneumococcal surface protein; vaccine; otitis media; meningitis; bacteraemia; pneumonia. |
| XX | |
| OS | Streptococcus pneumoniae; strain Bg7817. |
| XX | |
| PN | W09709994-AL. |
| XX | |
| XX | 20-MAR-1997. |
| PD | |
| XX | |
| PF | 16-SEP-1996; 96WO-US014819. |
| XX | |
| PR | 15-SEP-1995; 95US-00529055. |
| XX | |
| XX | (UABR-) UAB RES FOUND. |
| PA | |
| XX | |
| PI | Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ; |
| PI | Hollingshead S, Tart R, Brooks-Walter A; |
| XX | |
| DR | WPI; 1997-202002/18. |
| XX | |
| PT | Streptococcus pneumoniae surface protein PspC and truncated PspA - used |
| PT | in vaccines for protecting animals against S.pneumoniae infection. |
| XX | |
| PS | Example 6; Fig 13; 296pp; English. |
| XX | |
| CC | This sequence shows the central portion, including the C-terminus of the |
| CC | alpha-helix region and some of the proline-rich region, of pneumococcal |
| CC | surface protein A (PspA) of Streptococcus pneumoniae strain Bg7817. |
| CC | Comparison of the N-terminal and central regions (AAW14533-57 and |
| CC | AAW14562-91) of PspA polypeptides from different pneumococcal strains can |
| CC | be used to divide the strains into several families based on sequence |
| CC | homologies. PspA polypeptides, or fragments of them, can be used in |
| CC | vaccines to protect animals against S. pneumoniae infection and hence for |
| CC | the prevention of diseases such as otitis media, meningitis, bacteraemia |
| CC | and pneumonia. The sequence of the 3' half of the PspA alpha-helical |
| CC | region and the immediate 5' tip of the coding sequence are likely to be |
| CC | the critical sequences for predicting PspA cross-reactions and vaccine |
| CC | composition. (Updated on 17-OCT-2003 to standardise OS field) |
| XX | |
| SQ | Sequence 212 AA; |
| Query Match | 82.8%; Score 447; DB 2; Length 212; |
| Best Local Similarity | 86.1%; Pred. No. 1.4e-34; |
| Matches | 93; Conservative 4; Mismatches 11; Indels 0; Gaps 0; |
| Qy | 1 LEKAEAELENLLSTLDPGCKTQDELKGAAREAELENKKVEALPNPYKELEEEELSPEDNLK 60 |
| Db | 28 LEKAGAGLGNLLSTLDPGCKTQDELKGAAREAELENKKVEALPNPYKELEEEELSKLEDNK 87 |
| Qy | 61 DAETNHVEDYIKEGLEAEATKQAELEETPQBVDAALNDLVPDGGEE 108 |
| Db | 88 DAETNHVEDYIKEGLEAEATKQAELEETPKELDAALNELGPDGDEE 135 |
| RESULT 7 | |
| ABW02622 | |
| ID | ABW02622 standard; protein; 212 AA. |
| XX | |
| AC | ABW02622; |
| XX | |
| DT | 12-FEB-2004 (first entry) |
| XX | |
| DE | Bg7817c pneumococcal surface protein A (PspA) central region. |

Db 25 LEKAAEAELENLLSTLDPEGKTQDELDKAAEAEALNKKVEALPNQVSELEELSLEDNLK 84

Qy 61 DASTNHVEDYIKGLEEATATKQAELEETPOEVDAAALNDLVPPDGSEE 108
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 85 DASTNNVEDYIKGLEEATATKQAELEKTPKELDAAALNELGPDGDEE 132
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
 AAW14587
 ID AAW14587 standard; protein; 238 AA.
 XX AC AAW14587;
 XX XX
 AC XX
 DT 17-OCT-2003 (revised)
 DT 28-OCT-1997 (first entry)
 XX XX
 DE Streptococcus pneumoniae PspA central region.
 XX XX
 KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
 KW bacteraemia; pneumonia.
 XX OS
 OS Streptococcus pneumoniae; strain Bgl1703.
 XX XX
 PN WO9709994-A1.
 XX XX
 PD 20-MAR-1997.
 XX XX
 PF 16-SEP-1996; 96WO-US014819.
 XX XX
 PR 15-SEP-1995; 95US-00529055.
 XX XX
 XX (UABR-) UAB RES FOUND.
 PA PA
 PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 XX XX
 DR WPI; 1997-202002/18.
 XX XX
 PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used
 PT in vaccines for protecting animals against S.pneumoniae infection.
 XX XX
 PS Example 6; Fig 13; 296pp; English.
 XX XX
 CC This sequence shows the central portion, including the C-terminus of the
 CC alpha-helix region and some of the proline-rich region, of pneumococcal
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Bgl1703.
 CC Comparison of the N-terminal and central regions (AAW14533-57 and
 CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
 CC be used to divide the strains into several families based on sequence
 CC homologies. PspA polypeptides, or fragments of them, can be used in
 CC vaccines to protect animals against S. pneumoniae infection and hence for
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
 CC region and the immediate 5' tip of the coding sequence are likely to be
 CC the critical sequences for predicting PspA cross-reactions and vaccine
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)
 XX XX
 SQ Sequence 238 AA;

Query Match 85.4%; Score 461; DB 2; Length 238;
 Best Local Similarity 88.0%; Pred. No. 7.2e-36;
 Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LEKAAEAELENLLSTLDPEGKTQDELDKGAAEALNKKVEALPNQVSELEELSPPEDNLK 60

Db 25 LEKAAEAELENLLSTLDPEGKTQDELDKAAEAEALNKKVEALPNQVSELEELSLEDNLK 84
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DASTNHVEDYIKGLEEATATKQAELEETPOEVDAAALNDLVPPDGSEE 108
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 85 DASTNNVEDYIKGLEEATATKQAELEKTPKELDAAALNELGPDGDEE 132
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6

CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg7561c
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 185 AA;
Query Match 94.8%; Score 512; DB 7; Length 185;
Best Local Similarity 95.3%; Pred. No. 7.1e-41;
Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EKAAEAELENLSTLDPGGKTQDELKGAEEAELNKKVEALPNPVXLEEEELSPEDNLKD 61
: : |||||
DB 1 KQKVNLLENLSTLDPGGKTQDELKGAEEAELNKKVEALPNPVXLEEEELSPEDNLKD 60
QY 62 AETHNVEDYIKGLEEAEATKQAELEETPQEVDAALNDLVPDGGEE 108
: : |||||
DB 61 AETHNVEDYIKGLEEAEATKQAELEETPQEVDAALNDLVPDGGEE 107
RESULT 2
ABU08487
ID ABU08487 standard; protein; 8991 AA.
XX
AC ABU08487;
XX
DT 24-JUN-2003 (first entry)
XX
DE S. pneumoniae pneumococcal surface protein A (PspA) protein.
XX
KW Pneumococcal surface protein C; PspC; pneumococcal surface protein A;
KW alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;
KW antibacterial.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..8991
FT /note= "All Xaa residues within this sequence are
FT unknown"
XX
PN US6500613-B1.
XX
PD 31-DEC-2002.
XX
PF 16-SEP-1996; 96US-00714741.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UYAL-) UNIV ALABAMA.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
DR WPI; 2003-361534/34.
XX
PT Isolated PspC amino acid sequence used as polymerase chain reaction or
PT hybridization probe, comprises pneumococcal surface protein having alpha-
PT helical, proline rich and repeat regions.
XX
PS Disclosure; Col 145-188; 186pp; English.
XX
CC The present invention relates to the isolation of Streptococcus
CC pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide
CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-
CC like protein having alpha-helical, proline rich and repeat regions. The
CC PspC and PspA proteins may be used in a vaccine to protect against
CC pneumococcal infections. The polynucleotide sequences encoding PspC and
CC PspA may be used for the expression of the proteins, and as PCR primers
CC or hybridisation probes. The present sequence represents S. pneumoniae

CC PspA protein
XX
SQ Sequence 8991 AA;
Query Match 94.8%; Score 512; DB 6; Length 8991;
Best Local Similarity 95.3%; Pred. No. 8e-39; 3; Indels 0; Gaps 0;
Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EKAAEAELENLSTLDPGGKTQDELKGAEEAELNKKVEALPNPVXLEEEELSPEDNLKD 61
: : |||||
DB 8380 KQKVNLLENLSTLDPGGKTQDELKGAEEAELNKKVEALPNPVXLEEEELSPEDNLKD 8439
QY 62 AETHNVEDYIKGLEEAEATKQAELEETPQEVDAALNDLVPDGGEE 108
: : |||||
DB 8440 AETHNVEDYIKGLEEAEATKQAELEETPQEVDAALNDLVPDGGEE 8486
RESULT 3
AAW14589
ID AAW14589 standard; protein; 184 AA.
XX
AC AAW14589;
XX
DT 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Bg7561.
XX
FH Key Location/Qualifiers
FT Misc-difference 44
FT /note= "unidentified amino acid"
XX
PN WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
DR WPI; 1997-202002/18.
XX
PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
PS Example 6; Fig 13; 296pp; English.
XX
CC This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7561.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 184 AA;

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 76.7468 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-26

Perfect score: 540

Sequence: 1 LEKAEAELENLLTLDPGK.....TPQEVDAALNDIVPDGEE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 512 | 94.8 | 185 | 7 | ABW02623 Bg7561c p |
| 2 | 512 | 94.8 | 8991 | 6 | ABU08487 S. pneumo |
| 3 | 488.5 | 90.5 | 184 | 2 | AAW14589 Streptoco |
| 4 | 461 | 85.4 | 211 | 7 | ABW02621 Bg11703c |
| 5 | 461 | 85.4 | 238 | 2 | AAW14587 Streptoco |
| 6 | 447 | 82.8 | 212 | 7 | ABW02622 Bg7817c p |
| 7 | 447 | 82.8 | 212 | 7 | ABW02624 Bf5668c p |
| 8 | 414 | 76.7 | 232 | 7 | ABW02624 Bf5668c p |
| 9 | 414 | 76.7 | 275 | 8 | ADO52055 S. pneumo |
| 10 | 414 | 76.7 | 369 | 8 | ADK52496 alpha hel |
| 11 | 414 | 76.7 | 458 | 2 | AAW14592 Streptoco |
| 12 | 414 | 76.7 | 458 | 7 | ABW02626 Bf5668 pn |
| 13 | 414 | 76.7 | 653 | 8 | ADK52495 PspA mole |
| 14 | 414 | 76.7 | 653 | 8 | ADO52080 S. pneumo |
| 15 | 403.5 | 74.7 | 233 | 2 | AAW14590 Streptoco |
| 16 | 281 | 52.0 | 459 | 8 | ADO15316 S. pneumon |
| 17 | 270 | 50.0 | 213 | 7 | ABW02601 Bg8090c p |
| 18 | 259 | 48.0 | 213 | 7 | AAW14567 Streptoco |
| 19 | 258 | 47.8 | 416 | 8 | ADK52498 alpha hel |
| 20 | 258 | 47.8 | 526 | 8 | ADK52497 PspA mole |
| 21 | 258 | 47.8 | 744 | 6 | ABU00449 S. pneumo |
| 22 | 258 | 47.8 | 744 | 6 | ADM92054 S. pneumon |
| 23 | 258 | 47.8 | 745 | 3 | AAW81652 Streptoco |
| 24 | 257 | 47.6 | 641 | 2 | AAW61217 Streptoco |
| 25 | 257 | 47.6 | 641 | 5 | ABP54636 S. pneumo |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 26 | 257 | 47.6 | 641 | 7 | ADC45241 S. pneumo |
| 27 | 254 | 47.0 | 197 | 7 | ABW02598 Ac122c pn |
| 28 | 245 | 45.4 | 487 | 8 | ADR04321 Streptoco |
| 29 | 245 | 45.4 | 489 | 8 | ADO52088 Streptoco |
| 30 | 245 | 45.4 | 524 | 8 | ADO52082 E. coli B |
| 31 | 245 | 45.4 | 627 | 8 | ADO52129 E. coli B |
| 32 | 244 | 45.2 | 233 | 7 | ABW02606 Bf1019c p |
| 33 | 238 | 44.1 | 230 | 8 | ADO52086 S. pneumo |
| 34 | 238 | 44.1 | 230 | 8 | ADR04319 Streptoco |
| 35 | 238 | 44.1 | 290 | 8 | ADO52119 PYA3637 b |
| 36 | 238 | 44.1 | 298 | 8 | ADO52127 PYA3637 b |
| 37 | 237 | 43.9 | 233 | 2 | AAW14572 Streptoco |
| 38 | 236.5 | 43.8 | 196 | 2 | AAW14564 Streptoco |
| 39 | 231.5 | 42.9 | 119 | 2 | AAW46291 Pneumonoc |
| 40 | 231.5 | 42.9 | 215 | 2 | AAW14563 Streptoco |
| 41 | 231.5 | 42.9 | 215 | 7 | ABW02597 Atcc6303c |
| 42 | 167 | 30.9 | 204 | 2 | AAW14571 Streptoco |
| 43 | 167 | 30.9 | 204 | 7 | ABW02605 Bf1019c p |
| 44 | 167 | 30.9 | 289 | 2 | AAW62276 Streptoco |
| 45 | 167 | 30.9 | 289 | 2 | AAW41840 Streptoco |

ALIGNMENTS

RESULT 1
ABW02623
ID ABW02623 standard; protein; 185 AA.
XX AC ABW02623;
XX AC
DT 12-FEB-2004 (first entry)
XX DE Bg7561c pneumococcal surface protein A (PspA) central region.
XX DE
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX OS Unidentified.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 45
FT /label= Unknown
XX XX
PN US6592876-B1.
XX PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.
XX
XX Immunological composition for obtaining expression products used for
XX detecting the presence of Streptococcus pneumoniae or its strain,
XX comprises at least two different full length isolated gene encoding
XX pneumococcal surface protein A.
XX
XX Example 6; SEQ ID NO 69; 121pp; English.
XX
XX The present invention relates to an immunological composition comprising
XX at least 2 different full length isolated genes encoding pneumococcal
XX surface protein A (PspAs) from different groups based on restriction
XX fragment polymorphism analysis. The invention is useful for obtaining
XX expression products by recombinant techniques to detect, determine,
XX isolate or diagnose the presence of Streptococcus pneumoniae or its
XX strain. The expression product is useful for preparing antigenic,

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; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence
US-10-702-305A-18

Query Match          68.3%; Score 361.5; DB 16; Length 459;
Best Local Similarity 66.1%; Pred. No. 3.5e-18;
Matches 76; Conservative 13; Mismatches 15; Indels 11; Gaps 2;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAE-----AELNEKVEALONQVAELEEEELSKLE 56
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 345 LEDAELEKVLATLDPEGKTQDELDKAAEDANTEALQNKVADLENKVAEILDKEVTRIQ 404
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 57 DNLKDAETNNVEDYIKEGLEEAIAATKKALEKT-----OKELDAALNELGPDG 104
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 405 SOLKDAEENNVEDYKVEGLDKALTDKKVLENNNTQKALDTAOKALDTALNELGPDG 459
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-414-532-34
; Sequence 34, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; FILE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 34
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: sequence of codon optimized pspA-EF5668-Rx1
US-10-414-532-34

Query Match          61.0%; Score 322.5; DB 16; Length 487;
Best Local Similarity 72.1%; Pred. No. 2.4e-15;
Matches 75; Conservative 4; Mismatches 16; Indels 9; Gaps 2;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALONQVAELEEEELSKLEDNLK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 167 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALONQVAELEEEELSKLEDNLK 226
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DAET-----NNVEDYIKEGLEEAIAATKKALEKTQKELDAA 96
   ||||| : { ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 227 DAETLQSPVASQSKAEKDYDAAKDAKNAKKA-VEDAQKALDDA 269
   ||||| : { ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 15
US-10-414-533-21
; Sequence 21, Application US/10414533
; Publication No. US20040120962A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSES TO FOREIGN ANTIGENS EXPRESSED
; FILE OF INVENTION: BY RECOMBINANT ATTENUATED BACTERIAL VECTORS
; FILE REFERENCE: 56029-40420
; CURRENT APPLICATION NUMBER: US/10/414,533
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,676
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/373,669
; PRIOR FILING DATE: 2002-04-18
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-533-21

Query Match          61.0%; Score 322.5; DB 16; Length 487;
Best Local Similarity 72.1%; Pred. No. 2.4e-15;
Matches 75; Conservative 4; Mismatches 16; Indels 9; Gaps 2;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALONQVAELEEEELSKLEDNLK 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 167 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALONQVAELEEEELSKLEDNLK 226
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 DAET-----NNVEDYIKEGLEEAIAATKKALEKTQKELDAA 96
   ||||| : { ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 227 DAETLQSPVASQSKAEKDYDAAKDAKNAKKA-VEDAQKALDDA 269
   ||||| : { ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
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Search completed: November 17, 2005, 20:29:19
Job time : 72.832 secs

Db 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVQVALEEEELSKLEDNLK 335
QY 61 DAETNNVEDYIYKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
Db 336 DAETNNVEDYIYKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 383

RESULT 6
US-10-674-755-23
; Sequence 23, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-23

Query Match 91.3%; Score 483; DB 15; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.3e-27;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVQVALEEEELSKLEDNLK 60
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 60
QY 61 DAETNNVEDYIYKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
Db 61 DAETNNVEDYIYKEGLEEAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 7
US-10-299-636-82
; Sequence 82, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-82

Query Match 91.3%; Score 483; DB 15; Length 211;
Best Local Similarity 90.7%; Pred. No. 2.7e-27;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVQVALEEEELSKLEDNLK 60
Db 25 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 84
QY 61 DAETNNVEDYIYKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
Db 85 DAETNNVEDYIYKEGLEEAATKQAELEKTPKELDAALNELGPDGDEEE 132

RESULT 8
US-10-674-755-24
; Sequence 24, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-24

Query Match 88.3%; Score 467; DB 15; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.9e-26;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVQVALEEEELSKLEDNLK 60
Db 1 LEKAGAGLENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 60
QY 61 DAETNNVEDYIYKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
Db 61 DAETNNVEDYIYKEGLEEAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 9
US-10-299-636-83
; Sequence 83, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-83

Query Match 87.0%; Score 460; DB 15; Length 212;
Best Local Similarity 88.0%; Pred. No. 1.2e-25;

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US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-85

Query Match      100.0%; Score 529; DB 15; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.5e-30;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 60
|
Db 51 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 110
|
Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 108
|
Db 111 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 158
|

RESULT 3
US-10-414-532-1
; Sequence 1, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-1

Query Match      100.0%; Score 529; DB 16; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 60
Db 167 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 226
Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 108
|

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Db 227 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 274
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RESULT 4
US-10-299-636-88
; Sequence 88, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-88

Query Match      100.0%; Score 529; DB 15; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 60
|
Db 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 335
|
Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 108
|
Db 336 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEE 383
|

RESULT 5
US-10-414-532-26
; Sequence 26, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-26

Query Match      100.0%; Score 529; DB 16; Length 653;
Best Local Similarity 100.0%; Pred. No. 4.6e-30;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVAAEELSLEDNLK 60
|

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 71.832 Seconds
(without alignments)
629.082 Million cell updates/sec

Title: US-10-674-755-25
Perfect score: 529
Sequence: 1 LEDAELEKVLATLDPEGK.....TQKELDAALNELGPDGDEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 529 | 100.0 | 108 | 15 | US-10-674-755-25 |
| 2 | 529 | 100.0 | 232 | 15 | US-10-299-636-85 |
| 3 | 529 | 100.0 | 275 | 16 | US-10-414-532-1 |
| 4 | 529 | 100.0 | 458 | 15 | US-10-299-636-88 |
| 5 | 529 | 100.0 | 653 | 16 | US-10-414-532-26 |
| 6 | 483 | 91.3 | 108 | 15 | US-10-674-755-23 |
| 7 | 483 | 91.3 | 211 | 15 | US-10-299-636-82 |
| 8 | 467 | 88.3 | 108 | 15 | US-10-674-755-24 |
| 9 | 460 | 87.0 | 212 | 15 | US-10-299-636-83 |
| 10 | 455 | 86.0 | 106 | 15 | US-10-674-755-22 |
| 11 | 414 | 78.3 | 108 | 15 | US-10-674-755-26 |
| 12 | 395 | 74.7 | 185 | 15 | US-10-299-636-84 |
| 13 | 361.5 | 68.3 | 459 | 16 | US-10-702-305A-18 |
| 14 | 322.5 | 61.0 | 487 | 16 | US-10-414-532-34 |
| 15 | 322.5 | 61.0 | 487 | 16 | US-10-414-532-21 |
| 16 | 322.5 | 61.0 | 524 | 16 | US-10-414-532-28 |
| 17 | 322 | 60.9 | 744 | 10 | US-09-769-787-184 |
| 18 | 322 | 60.9 | 744 | 17 | US-10-472-928-32 |
| 19 | 321 | 60.7 | 641 | 9 | US-09-765-272-160 |
| 20 | 321 | 60.7 | 641 | 20 | US-11-106-649-160 |
| 21 | 315 | 59.5 | 104 | 15 | US-10-674-755-21 |
| 22 | 313 | 59.2 | 104 | 15 | US-10-674-755-20 |
| 23 | 311.5 | 58.9 | 290 | 16 | US-10-414-532-65 |
| 24 | 308 | 58.2 | 230 | 16 | US-10-414-532-32 |
| 25 | 308 | 58.2 | 230 | 16 | US-10-414-533-19 |
| 26 | 306 | 57.8 | 197 | 15 | US-10-299-636-59 |
| 27 | 305 | 57.7 | 213 | 15 | US-10-299-636-62 |
| 28 | 298.5 | 56.4 | 119 | 15 | US-10-674-755-27 |
| 29 | 298.5 | 56.4 | 215 | 15 | US-10-299-636-58 |
| 30 | 293 | 55.4 | 102 | 15 | US-10-674-755-18 |
| 31 | 282.5 | 53.4 | 233 | 15 | US-10-299-636-67 |
| 32 | 233 | 44.0 | 80 | 15 | US-10-674-755-19 |
| 33 | 206 | 38.9 | 354 | 15 | US-10-299-636-105 |
| 34 | 206 | 38.9 | 588 | 15 | US-10-299-636-96 |
| 35 | 206 | 38.9 | 619 | 10 | US-09-882-774-1 |
| 36 | 206 | 38.9 | 619 | 15 | US-10-282-122A-73702 |
| 37 | 206 | 38.9 | 619 | 16 | US-10-414-532-72 |
| 38 | 205 | 38.8 | 204 | 15 | US-10-299-636-66 |
| 39 | 201 | 38.0 | 99 | 15 | US-10-674-755-11 |
| 40 | 197.5 | 37.3 | 100 | 15 | US-10-674-755-12 |
| 41 | 196 | 37.1 | 198 | 15 | US-10-299-636-76 |
| 42 | 185 | 35.0 | 141 | 14 | US-10-254-995-2 |
| 43 | 185 | 35.0 | 589 | 9 | US-09-748-875-14 |
| 44 | 185 | 35.0 | 589 | 10 | US-09-298-523B-14 |
| 45 | 185 | 35.0 | 589 | 15 | US-10-299-636-97 |

ALIGNMENTS

RESULT 1
US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-25

Query Match 100.0%; Score 529; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.5e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELKKEAAEALNEKVEALQNOVAEELEESKLEDNLK 60
Db 1 LEDAELEKVLATLDPEGKTQDELKKEAAEALNEKVEALQNOVAEELEESKLEDNLK 60
Qy 61 DAETNNVEDYIKEGLEEAIAATKKALEKTKQELDAALNELGPDGDEEE 108
Db 61 DAETNNVEDYIKEGLEEAIAATKKALEKTKQELDAALNELGPDGDEEE 108

RESULT 2

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; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-22

Query Match      86.0%; Score 455; DB 4; Length 106;
Best Local Similarity 89.8%; Pred. No. 2.4e-32;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAAEEELSLEDNLK 60
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQV-ELEEELSLEDNLK 59
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 108
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 14
US-08-710-749-25
; Sequence 25, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-25

Query Match      78.3%; Score 414; DB 2; Length 108;
Best Local Similarity 79.6%; Pred. No. 8.2e-29;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAAEEELSLEDNLK 60
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQV-ELEEELSLEDNLK 60
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 108
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEBTPQEVDAALNDLVPDGGEEE 108
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

RESULT 15

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US-09-147-875A-26
; Sequence 26, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(108)
; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
US-09-147-875A-26

Query Match      78.3%; Score 414; DB 4; Length 108;
Best Local Similarity 79.6%; Pred. No. 8.2e-29;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAAEEELSLEDNLK 60
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQV-ELEEELSLEDNLK 60
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTQKELDAALNELGPDGDEEE 108
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEBTPQEVDAALNDLVPDGGEEE 108
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Search completed: November 17, 2005, 19:32:23
Job time : 21.9185 secs
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-68

Query Match      87.0%; Score 460; DB 4; Length 212;
Best Local Similarity 88.0%; Pred. No. 1.9e-32;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDEKAAEAELNEKVEALQNOVAELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 28 LEKAGAGLGNLLSTLDPEGKTQDELDEKAAEAELNKKVEALPNQVSELEEEELSKLEDNLK 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKQKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 88 DAETNNVEDYIKEGLEEAIAATKAELEKTKPKELDAALNELGPDGDEEE 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-23

Query Match      86.4%; Score 457; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.6e-32;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDEKAAEAELNEKVEALQNOVAELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 LEKAGAGLGNLLSTLDPEGKTQDELDEKAAEAELNKKVEALPNQVSELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKQKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKPKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-147-875A-22
; Sequence 22, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-68

Query Match      87.0%; Score 460; DB 4; Length 212;
Best Local Similarity 88.0%; Pred. No. 1.9e-32;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDEKAAEAELNEKVEALQNOVAELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 28 LEKAGAGLGNLLSTLDPEGKTQDELDEKAAEAELNKKVEALPNQVSELEEEELSKLEDNLK 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKQKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 88 DAETNNVEDYIKEGLEEAIAATKAELEKTKPKELDAALNELGPDGDEEE 135
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-23

Query Match      86.4%; Score 457; DB 2; Length 108;
Best Local Similarity 87.0%; Pred. No. 1.6e-32;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDEKAAEAELNEKVEALQNOVAELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 LEKAGAGLGNLLSTLDPEGKTQDELDEKAAEAELNKKVEALPNQVSELEEEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKQKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DAETNNVEDYIKEGLEEAIAATKAELEKTKPKELDAALNELGPDGDEEE 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-147-875A-22
; Sequence 22, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
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Query Match          91.3%; Score 483; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 9.3e-35;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEELEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-08-529-055-67
; Sequence 67, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-67

Query Match          91.3%; Score 483; DB 4; Length 211;
Best Local Similarity 90.7%; Pred. No. 2e-34;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEELEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Query Match          88.3%; Score 467; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 2.2e-33;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEELEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LEKAGAGLENLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEELSKLEDNLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DAETNNVEDYIKEGLEEAIAATKKALEKTQKELDAALNELGPDGDEEE 108
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RESULT 10
US-08-529-055-68
; Sequence 68, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-67
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Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 60
|||||
Db 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 335
|||||

QY 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 108
|||||
Db 336 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 383
|||||

RESULT 5
US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 100.0%; Score 529; DB 4; Length 8991;
Best Local Similarity 100.0%; Pred. No. 1.7e-36;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 60
|||||
Db 8615 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 8674
|||||

QY 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 108
|||||
Db 8675 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 8722
|||||

RESULT 6
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match 91.3%; Score 483; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 9.3e-35;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 60
|||||
Db 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNEKVEALPNQVSELEEEELSKLEDNLK 60
|||||

QY 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 108
|||||
Db 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEE 108
|||||

RESULT 7
US-09-147-875A-23
; Sequence 23, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-23

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 20.7935 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-25
Perfect score: 529
Sequence: 1 LEDAELEKVLATLDPEGK.....TQKELDAALNELGPDGDEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 529 | 100.0 | 108 | 2 | US-08-710-749-24 |
| 2 | 529 | 100.0 | 108 | 4 | US-09-147-875A-25 |
| 3 | 529 | 100.0 | 232 | 4 | US-08-529-055-70 |
| 4 | 529 | 100.0 | 458 | 4 | US-08-529-055-73 |
| 5 | 529 | 100.0 | 8991 | 4 | US-08-714-741-32 |
| 6 | 483 | 91.3 | 108 | 2 | US-08-710-749-26 |
| 7 | 483 | 91.3 | 108 | 4 | US-09-147-875A-23 |
| 8 | 483 | 91.3 | 211 | 4 | US-08-529-055-67 |
| 9 | 467 | 88.3 | 108 | 4 | US-09-147-875A-24 |
| 10 | 460 | 87.0 | 212 | 4 | US-08-529-055-68 |
| 11 | 457 | 86.4 | 108 | 2 | US-08-710-749-22 |
| 12 | 457 | 86.4 | 108 | 2 | US-08-710-749-23 |
| 13 | 455 | 86.0 | 106 | 4 | US-09-147-875A-22 |
| 14 | 414 | 78.3 | 108 | 2 | US-08-710-749-25 |
| 15 | 414 | 78.3 | 108 | 4 | US-09-147-875A-26 |
| 16 | 395 | 74.7 | 185 | 4 | US-08-529-055-69 |
| 17 | 321 | 60.7 | 641 | 3 | US-08-961-083-160 |
| 18 | 321 | 60.7 | 641 | 4 | US-09-536-784-160 |
| 19 | 315 | 59.5 | 104 | 4 | US-09-147-875A-21 |
| 20 | 313 | 59.2 | 104 | 2 | US-08-710-749-19 |
| 21 | 313 | 59.2 | 104 | 4 | US-09-147-875A-20 |
| 22 | 309 | 58.4 | 104 | 2 | US-08-710-749-20 |
| 23 | 306 | 57.8 | 197 | 4 | US-08-529-055-44 |
| 24 | 305 | 57.7 | 213 | 4 | US-08-529-055-47 |
| 25 | 298.5 | 56.4 | 119 | 2 | US-08-710-749-27 |
| 26 | 298.5 | 56.4 | 119 | 4 | US-09-147-875A-27 |
| 27 | 298.5 | 56.4 | 215 | 4 | US-08-529-055-43 |

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| 28 | 293 | 55.4 | 102 | 2 | US-08-710-749-21 | Sequence 21, Appl |
| 29 | 293 | 55.4 | 102 | 4 | US-09-147-875A-18 | Sequence 18, Appl |
| 30 | 282.5 | 53.4 | 233 | 4 | US-08-529-055-52 | Sequence 52, Appl |
| 31 | 233 | 44.0 | 80 | 2 | US-08-710-749-18 | Sequence 18, Appl |
| 32 | 233 | 44.0 | 80 | 4 | US-09-147-875A-19 | Sequence 19, Appl |
| 33 | 212.5 | 40.2 | 289 | 1 | US-08-072-070-4 | Sequence 4, Appl |
| 34 | 212.5 | 40.2 | 289 | 1 | US-08-469-434-4 | Sequence 4, Appl |
| 35 | 212.5 | 40.2 | 289 | 1 | US-08-214-222-4 | Sequence 4, Appl |
| 36 | 212.5 | 40.2 | 289 | 2 | US-08-467-852A-5 | Sequence 5, Appl |
| 37 | 212.5 | 40.2 | 289 | 2 | US-08-468-718-4 | Sequence 4, Appl |
| 38 | 212.5 | 40.2 | 289 | 2 | US-08-247-491A-5 | Sequence 5, Appl |
| 39 | 206 | 38.9 | 288 | 3 | US-08-312-949-4 | Sequence 4, Appl |
| 40 | 206 | 38.9 | 288 | 3 | US-08-446-201-4 | Sequence 4, Appl |
| 41 | 206 | 38.9 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |
| 42 | 206 | 38.9 | 619 | 1 | US-08-214-164-2 | Sequence 2, Appl |
| 43 | 206 | 38.9 | 619 | 2 | US-08-467-852A-3 | Sequence 3, Appl |
| 44 | 206 | 38.9 | 619 | 2 | US-08-246-636-2 | Sequence 2, Appl |
| 45 | 206 | 38.9 | 619 | 2 | US-08-247-491A-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-08-710-749-24
; Sequence 24, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Brilles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Curtis, Morris & Safford
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710.749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/POCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-24

Query Match 100.0%; Score 529; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1e-38;
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Db 1 LEDAELEKVLATLDPEGKTQDELDKAAAEELNEKVEALQNVAELEBELSKLEDNLK 60

Search completed: November 17, 2005, 20:37:53
Job time : 64.0187 secs

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Matches 76; Conservative 14; Mismatches 18; Indels 11; Gaps 2;

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Db 51 LEXAAEELENLSTLDPEGKTQDELDEKEAAEDANIEALQNKVADLENKVAELDKVETRLQ 110
   ||| :||| :|||||:|||||:| | | | | | | | | | | | | | | | | | | | |

Qy 57 DNLKDAETNNVEDYIKGLEBAIATKKAEELEKT-----QKELDAAINELPGDGDEE 108
   :|||||:|||||:|||||:| | | | | | | | | | | | | | | | | | | | |
Db 111 SDLKDABENNVEDYVKEGLEKALTDDKKVELNNTQKALDTAQKALDTALNELPGDGDEE 169
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RESULT 13
Q9L562 PRELIMINARY; PRT; 242 AA.
AC Q9L562;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBurel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBurel. 26, Last annotation update)
DE PEpa (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=69;
RC MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RJ J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=69;
RC Beall B.W.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL: AF255908; AAF70098.1; -.
FT NON_TER      1          1
FT NON_TER     242        242
SQ SEQUENCE    242 AA; 25843 MW; 707EA930797D2C82 CRC64;

Query Match           64.1%; Score 339; DB 2; Length 242;
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Matches 75; Conservative 13; Mismatches 16; Indels 4; Gaps 2;

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Db 70 LAKKQTEKLXSLSDPEGKTQDELDEKEAAEELDKKVEALQNKVADLEKESINLEILG 129
   ||| :||| :|||||:|||||:| | | | | | | | | | | | | | | | | | | | |

Qy 61 DAETNNVEDYIKGLEBAIATKKAEELEKTOKELDDAALNELPGDGDEE 108
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Db 130 GADS---ED-DTAAQLNQKLATTKKAEELEKTOKELDDAALNELPGDGDEE 173
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RESULT 14
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ID Q9L584
AC Q9L584;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBurel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBurel. 25, Last annotation update)
DE PEpa (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6303;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/JAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
in Streptococcus pneumoniae."
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071820; AAF2715.1; -.
FT NON TER 461
SQ SEQUENCE 461 AA; 51563 MW; 249435F65585BB92 CRC64;

Query Match 72.9%; Score 385.5; DB 2; Length 461;
Best Local Similarity 68.1%; Pred. No. 1.9e-13;
Matches 81; Conservative 12; Mismatches 15; Indels 11; Gaps 2;

Oy 1 LEDAELEKVLATLDPEGKTQDELDKAAE-----AELNEKVEALQNOVALEELSLE 56
Db 273 LEDAELEKVLATLDPEGKTQDELDKAAEDANTEALQNKVADLENKVAELDKVETRLQ 332
Oy 57 DNLKDAETNNVEDYIKEGLEEAIAATKKAELEKT-----KELDAALNELGPDGDEE 108
Db 333 SOLKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAKALDTALNELGPDGDEE 391

RESULT 10
O9KGS0 PRELIMINARY; PRT; 227 AA.
AC O9KGS0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA protein (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
pneumococcal strains in the United States and of internationally
disseminated clones."
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288751; AAF91495.1; -.
FT NON TER 1
FT NON TER 227
SQ SEQUENCE 227 AA; 24994 MW; 9D24C706228052A6 CRC64;

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Best Local Similarity 67.2%; Pred. No. 1.4e-13;
Matches 80; Conservative 13; Mismatches 15; Indels 11; Gaps 2;

Oy 1 LEDAELEKVLATLDPEGKTQDELDKAAE-----AELNEKVEALQNOVALEELSLE 56
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Query Match 72.9%; Score 362.5; DB 2; Length 211;
Best Local Similarity 63.9%; Pred. No. 1.6e-12;
Matches 76; Conservative 14; Mismatches 18; Indels 11; Gaps 2;

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Db 5 LEKAELENLLSTLDPEGKTQDELDKAAEDVNIEALQNKVADLENKVAELDKVETRLQ 64
Oy 57 DNLKDAETNNVEDYIKEGLEEAIAATKKAELEKT-----KELDAALNELGPDGDEE 108
Db 65 SDKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAKALDTALNELGPDGDEE 123

RESULT 11
O9KGS0 PRELIMINARY; PRT; 211 AA.
AC O9KGS0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP95;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicunzo G., Gherardi G., Getz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
Italian patients."
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490265; AAN37733.1; -.
FT NON TER 1
FT NON TER 211
SQ SEQUENCE 211 AA; 23207 MW; 096BFEB08CD6483 CRC64;

Query Match 68.5%; Score 362.5; DB 2; Length 211;
Best Local Similarity 63.9%; Pred. No. 1.6e-12;
Matches 76; Conservative 14; Mismatches 18; Indels 11; Gaps 2;

Oy 1 LEDAELEKVLATLDPEGKTQDELDKAAE-----AELNEKVEALQNOVALEELSLE 56
Db 5 LEKAELENLLSTLDPEGKTQDELDKAAEDVNIEALQNKVADLENKVAELDKVETRLQ 64
Oy 57 DNLKDAETNNVEDYIKEGLEEAIAATKKAELEKT-----KELDAALNELGPDGDEE 108
Db 65 SDKDAEENNVEDYIKEGLEKALTDKKVELNNTQKALDTAKALDTALNELGPDGDEE 123

RESULT 12
O9L594 PRELIMINARY; PRT; 257 AA.
AC O9L594;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
pneumococcal strains in the United States and of internationally
disseminated clones."
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX Beall B.W.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF254255; AAF68090.1; -.
DR

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RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
J. Clin. Microbiol. 40:3660-3665 (2002).
DR ENBL; AF490268; AAN37736.1; -.
FT NON_TER 1 213
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 23490 MW; 23B4428409526EAB CRC64;

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Best Local Similarity 88.0%; Pred. No. 3.8e-18;
Matches 95; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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Db 26 LEXAEELENLLSLDPEGTQDELQKETAEAEINKKVQALONQVAELESELSKLEDNLK 85
   ||| | :||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 61 DAETNNVEDYIKGLEBEAIATKAEELEKTOKELDAAINELGPDGDDEE 108
   ||| | :||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 86 VAETNNVEDYIKGLEBEAIATKAEELEKTOKALDTALNELGPDGDDEE 133
   ||| | :||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 8
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ID Q9L595 PRELIMINARY; PRT; 256 AA.
AC Q9L595; AC Q9L595;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
J. Clin. Microbiol. 38:3663-3669 (2000).
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RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
J. Clin. Microbiol. 38:3663-3669 (2000).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RA Beall B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF254254; AAP68089.1; -.
FT NON_TER 1 256
FT NON_TER 256 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match      72.9%; Score 385.5; DB 2; Length 256;
Best Local Similarity 68.1%; Pred. No. 1.1e-13;
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Qy 1 LEDAELEKVLATLDPEGTQDELQKEAAE----HELNKVEALQNQVAELESELSKLE 56
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Db 52 LEDAELEKVLATLDPEGTQDELQKEAADANIQAALQNKVADLENKNVAELDKVTRLQ 111
   ||| | :||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 57 DNLKDAETNNVEDYIKGLEBEATATKAEELEKT-----QKELDAALNELGPDGDDEE 108
   ||| | :||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 112 SDLKDAETNNVEDYIKGLEBEATDKKVELNNTQKALDTAQAKALDTALNELGPDGDDEE 170
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RESULT 9
Q9LAX6 PRELIMINARY; PRT; 461 AA.
ID Q9LAX6 PRELIMINARY; PRT; 461 AA.
AC Q9LAX6; AC Q9LAX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

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OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP198;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Cherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP198;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF253408; AAF67356.1; -.
DR HSP; P05412; 1JNN.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26972 MW; 2190EED1460D26D9 CRC64;

Query Match 94.9%; Score 502; DB 2; Length 246;
Best Local Similarity 94.4%; Pred. No. 5.6e-20;
Matches 102; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 52 LEKAAELENLSTLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 111
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKGLEEAEIATKKALEKTKQELDAALNELGPDGDEEE 108
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 112 DAETNNVEDYIKGLEEAEIATKKALEKTKQELDAALNELGPDGDEEE 159
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
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AC Q9LAX2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG7817;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of pspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071826; AAF27719.1; -.
DR PRINTS; PR00194; TROPOMYCIN.
FT NON_TER 479
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SQ SEQUENCE 479 AA; 53257 MW; B9C0D2CA15DE3654 CRC64;

Query Match 94.1%; Score 498; DB 2; Length 479;
Best Local Similarity 93.5%; Pred. No. 1.7e-19;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 295 LEKAAELENLSTLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 354
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9LAX5 ID Q9LAX5 PRELIMINARY; PRT; 481 AA.
AC Q9LAX5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG11703;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of pspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071821; AAF27716.1; -.
DR HSP; P58301; 1L6D.
FT NON_TER 481
FT NON_TER 481
SQ SEQUENCE 481 AA; 53500 MW; EA3C66445EFC2B CRC64;

Query Match 94.1%; Score 498; DB 2; Length 481;
Best Local Similarity 93.5%; Pred. No. 1.7e-19;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 295 LEKAAELENLSTLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 354
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q8KQK2 ID Q8KQK2 PRELIMINARY; PRT; 107 AA.
AC Q8KQK2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Pneumococcal surface protein A (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255/00;
RX MEDLINE=22170754; PubMed=12183557;
RX DOI=10.1128/IAI.70.9.5086-5090.2002;
RA Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C.,
RA Dias W.O., Leite L.C.C.;
RT "Analysis of serum cross-reactivity and cross-protection elicited by
RT immunization with DNA vaccines against Streptococcus pneumoniae
RT expressing pspA fragments from different clades.";
RL Infect. Immun. 70:5086-5090(2002).
DR EMBL; AY082390; AAL92495.1; -.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

```

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Qy 61 DAETNNVEDYIKGLEEAEIATKKALEKTKQELDAALNELGPDGDEEE 108
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db .355 DAETNNVEDYIKGLEEAEIATKKALEKTKQELDAALNELGPDGDEEE 402
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9LAX5 ID Q9LAX5 PRELIMINARY; PRT; 481 AA.
AC Q9LAX5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BG11703;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of pspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071821; AAF27716.1; -.
DR HSP; P58301; 1L6D.
FT NON_TER 481
FT NON_TER 481
SQ SEQUENCE 481 AA; 53500 MW; EA3C66445EFC2B CRC64;

Query Match 94.1%; Score 498; DB 2; Length 481;
Best Local Similarity 93.5%; Pred. No. 1.7e-19;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 295 LEKAAELENLSTLDPEGKTQDELKKAEEAEAELEKVEALQNVAAEELEELSKLEDNLK 354
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q8KQK2 ID Q8KQK2 PRELIMINARY; PRT; 107 AA.
AC Q8KQK2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Pneumococcal surface protein A (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255/00;
RX MEDLINE=22170754; PubMed=12183557;
RX DOI=10.1128/IAI.70.9.5086-5090.2002;
RA Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C.,
RA Dias W.O., Leite L.C.C.;
RT "Analysis of serum cross-reactivity and cross-protection elicited by
RT immunization with DNA vaccines against Streptococcus pneumoniae
RT expressing pspA fragments from different clades.";
RL Infect. Immun. 70:5086-5090(2002).
DR EMBL; AY082390; AAL92495.1; -.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:32:37 ; Search time 64.0187 Seconds
(without alignments)
863.882 Million cell updates/sec

Title: US-10-674-755-25
Perfect score: 529
Sequence: 1 LEDALELEKVLATLDPEGK.....TQKELDAALNELPGDGDDEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|-------------|
| 1 | 529 | 100.0 | 653 | 034097 | streptococc |
| 2 | 502 | 94.9 | 246 | 0915B4 | streptococc |
| 3 | 498 | 94.1 | 479 | 091AX2 | streptococc |
| 4 | 498 | 94.1 | 481 | 091AX5 | streptococc |
| 5 | 497 | 94.0 | 107 | 08KQK2 | streptococc |
| 6 | 473 | 89.4 | 480 | 091AX3 | streptococc |
| 7 | 467 | 88.3 | 213 | 08GNS7 | streptococc |
| 8 | 385.5 | 72.9 | 256 | 091595 | streptococc |
| 9 | 385.5 | 72.9 | 461 | 091AX6 | streptococc |
| 10 | 382.5 | 72.3 | 227 | 09KGS0 | streptococc |
| 11 | 362.5 | 68.5 | 211 | 08GNT0 | streptococc |
| 12 | 362.5 | 68.5 | 257 | 091594 | streptococc |
| 13 | 339 | 64.1 | 242 | 091562 | streptococc |
| 14 | 326.5 | 61.7 | 222 | 091584 | streptococc |
| 15 | 324 | 61.2 | 231 | 091579 | streptococc |
| 16 | 324 | 61.2 | 241 | 091580 | streptococc |
| 17 | 322 | 60.9 | 228 | 0915B8 | streptococc |
| 18 | 322 | 60.9 | 235 | 091582 | streptococc |
| 19 | 322 | 60.9 | 249 | 0915D4 | streptococc |
| 20 | 322 | 60.9 | 252 | 091583 | streptococc |
| 21 | 322 | 60.9 | 360 | 08KQK3 | streptococc |
| 22 | 322 | 60.9 | 429 | 091AX7 | streptococc |
| 23 | 322 | 60.9 | 526 | 091AX9 | streptococc |
| 24 | 322 | 60.9 | 608 | 08VQ55 | streptococc |
| 25 | 322 | 60.9 | 744 | 097T39 | streptococc |
| 26 | 320 | 60.5 | 249 | 0915B7 | streptococc |
| 27 | 320 | 60.5 | 502 | 091AX8 | streptococc |
| 28 | 319 | 60.3 | 249 | 091585 | streptococc |
| 29 | 319 | 60.3 | 256 | 091590 | streptococc |
| 30 | 312.5 | 59.1 | 209 | 091593 | streptococc |
| 31 | 215 | 40.6 | 417 | 091AY3 | streptococc |

32 206 38.9 619 2 Q54972 streptococc
33 206 38.9 619 2 Q8DR10 streptococc
34 195 36.9 415 2 Q9LAY1 streptococc
35 185 35.0 739 2 Q9RQT4 streptococc
36 185 35.0 820 2 Q9RQT1 streptococc
37 185 35.0 929 2 Q9KK19 streptococc
38 185 35.0 929 2 Q9ZAY5 streptococc
39 178 33.6 249 2 Q9L575 streptococc
40 172 32.5 99 2 Q8KQK4 streptococc
41 172 32.5 395 2 Q9LAY2 streptococc
42 172 32.5 408 2 Q9LAY0 streptococc
43 171 32.3 426 2 Q9LAY5 streptococc
44 170 32.1 224 2 Q8GNS8 streptococc
45 168.5 31.9 869 2 Q9KK27 streptococc

ALIGNMENTS

RESULT 1
O34097 PRELIMINARY; PRT; 653 AA.
AC O34097;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DE PspA.
DE PspA.
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF5668;
RA MEDLINE=98427139; PubMed=9746574;
RX McDaniel L.S.; McDaniel D.O.; Hollingshead S.K.; Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
to the previously identified PspA sequence from strain Rx1 and ability
of PspA from EF5668 to elicit protection against pneumococci of
RT different capsular types.";
RL Infect. Immun. 66:4748-4754 (1998).
DR EMBL; U89711; AAC62252.1; -.
DR HSSP; P06653; 1HCX.
DR InterPro; IPR002479; CW binding.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR009053; Prefoldin.
DR Pfam; PF01473; CW_binding_1; 9.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
SQ SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;
Query Match 100.0%; Score 529; DB 2; Length 653;
Best Local Similarity 100.0%; Pred. No. 4.9e-21;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEDALELEKVLATLDPEGKTQDELDEKAAAEALNEKVAELQNVAELEELSKLEDNLK 60
|||||
Db 276 LEDALELEKVLATLDPEGKTQDELDEKAAAEALNEKVAELQNVAELEELSKLEDNLK 335
Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELPGDGDDEE 108
|||||
Db 336 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELPGDGDDEE 383
RESULT 2
Q915B4 PRELIMINARY; PRT; 246 AA.
ID Q915B4
AC Q915B4;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE PspA (fragment).
GN Name=pspA;

Job time : 15.1144 secs

C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004
C:Accession: J38055; JH0154; S12459; S09332; A30220; S49478
R:Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Stedman, H.H.
Eur. J. Biochem. 230, 1001-1006, 1995
A>Title: Characterization of a human perinatal myosin heavy-chain transcript.
A:Reference number: J38055; MUID:95324556; PMID:7601129
A:Accession: J38055
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1937 <RES>
A:Cross-references: UNIPROT:P13535; EMBL:Z38133; NID:g558668; PIDN:CAA86293.1; PID:g5586
R:Karsch-Mizrachi, I.; Peghali, R.; Shows, T.B.; Leinwand, L.A.
Gene 89, 289-294, 1990
A>Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.
A:Reference number: JH0154; MUID:902323631; PMID:2373371
A:Accession: JH0154
A:Molecule type: mRNA
A:Residues: 1-14, 'A', 16-859 <KAR>
A:Cross-references: GB:Y00821
A:Experimental source: skeletal muscle
R:Bober, E.
submitted to the EMBL Data Library, January 1989
A:Reference number: S12458
A:Accession: S12459
A:Molecule type: mRNA
A:Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>
A:Cross-references: EMBL:X51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A:Experimental source: clone gWHC-F
R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A>Title: Identification of three developmentally controlled isoforms of human myosin hea
A:Reference number: S09331; MUID:90235862; PMID:1691980
A:Accession: S09332
A:Molecule type: mRNA
A:Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 899-
1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668-17
A:Cross-references: EMBL:X51592
R:Feghali, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A>Title: Molecular genetic characterization of a developmentally regulated human perinat
A:Reference number: A30220; MUID:89234168; PMID:2715179
A:Accession: A30220
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-184
A:Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
C:Genetics:
A:Gene: GDB:MYH8
A:Cross-references: GDB:125267; OMIM:160741
A:Map position: 17pter-17p12
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F:91-769/Domain: myosin motor domain homology <MMOT>
F:91-188/Region: nucleotide-binding motif A (P-loop)
F:551-588/Region: actin binding #status predicted
F:658-680/Region: actin binding #status predicted
F:842-1282/Region: S2 #status predicted
F:698,708/Active site: Cys #status predicted

Query Match 21.6%; Score 114.5; DB 2; Length 1937;
Best Local Similarity 34.8%; Pred. No. 20;
Matches 40; Conservative 19; Mismatches 43; Indels 13; Gaps 4;
Qy 7 ELEKVLATLDP-
Db 847 ETEKMATMKEEFQTKDELAKSEAKRKELEEKVMTLLKKNKNDLQVQSEADSLADAE 906
Qy 65 N-----NVEDYIKGEELEAIAATKK--AELEKTQKELDAALNELGPDGDEE 108
Db 907 REQLIKNKIQLEAKIKVTERAEEREEINAEELTAKKRKLEDECSLEKDKIDDL 961

RESULT 13
JC5421
smooth muscle myosin heavy chain 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
R:Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A>Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains.
A:Reference number: JC5420; MUID:97242182; PMID:9125171
A:Accession: JC5421
A:Molecule type: mRNA
A:Residues: 1-1938 <HAS>
A:Cross-references: UNIPROT:O08638; DDBJ:D85924; NID:g1945079; PIDN:BAAL19691.1; PID:g194
C:Experimental source: smooth muscle
C:Comment: This protein plays a role in smooth muscle cell contraction.
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:88-771/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 21.6%; Score 114; DB 2; Length 1938;
Best Local Similarity 33.9%; Pred. No. 21;
Matches 43; Conservative 16; Mismatches 42; Indels 26; Gaps 5;
Qy 2 EDAAELEKVLATLDP-
Db 1559 EDAKLRLEVNQAL-
Qy 53 -----SKLENDLKDAETNNVEDYIKGEELEAIAATKK---AELEKTQKELD---AALNELG 101
Db 1615 AAAAKKLEGLDKOLELQ--ADSAIKGFEAAIKQLRKLAQMKQFQRELDARASDRIF 1672
Qy 102 PDGDEEE 108
Db 1673 ATSKENE 1679

RESULT 14
JC5420
smooth muscle myosin heavy chain 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5420
R:Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A>Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains.
A:Reference number: JC5420; MUID:97242182; PMID:9125171
A:Accession: JC5420
A:Molecule type: mRNA
A:Residues: 1-1972 <HAS>
A:Cross-references: UNIPROT:O08638; DDBJ:D85923; NID:g1945077; PIDN:BAAL19690.1; PID:g194
C:Experimental source: smooth muscle
C:Comment: This protein plays a role in smooth muscle cell contraction.
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:88-771/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 21.6%; Score 114; DB 2; Length 1972;
Best Local Similarity 33.9%; Pred. No. 22;
Matches 43; Conservative 16; Mismatches 42; Indels 26; Gaps 5;
Qy 2 EDAAELEKVLATLDP-
Db 1559 EDAKLRLEVNQAL-
Qy 53 -----SKLENDLKDAETNNVEDYIKGEELEAIAATKK---AELEKTQKELD---AALNELG 101
Db 1615 AAAAKKLEGLDKOLELQ--ADSAIKGFEAAIKQLRKLAQMKQFQRELDARASDRIF 1672
Qy 102 PDGDEEE 108
Db 1673 ATSKENE 1679

A:Accession: S07827
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 176-621 <BA2>
A:Cross-references: EMBL:X16262
A:Experimental source: Sprague-Dawley; smooth muscle; clone RAMHC21
C:Comment: For an alternate splice form see (PIRS07537).
C:Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 21.7%; Score 115; DB 2; Length 621;
Best Local Similarity 33.9%; Pred. No. 6;
Matches 43; Conservative 16; Mismatches 42; Indels 26; Gaps 5;

Qy 2 EDAAELEKVLATLDPDGKTDQLDKEAAAEALNEKVEALQNVAALEEL-----52
Db 208 EDAAKLRLEVMQAL-----KGQFDRDQARDEQNEEKRRQLRQLHVEYTELEDERKQRAL 263
Qy 53 -----SKLEDNLKDAETNNVEDYIKEGLEEAIAATKK---AALEKTKQKELD---RALNELG 101
Db 264 AAAAKKLEGGDLKLELQ---ADSAVKGREEAIKQLKLAQKQKQFRELDDARASRDEIF 321
Qy 102 PDGDEE 108
Db 322 ATSKENE 328

RESULT 9
S29795
hypothetical protein 2280 - evening primrose (Oenothera picensis subsp. picensis) chloro
C:Species: chloroplast Oenothera picensis subsp. picensis (evening primrose)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29795; S19983
R:Nimzyk, R.; Schoendorf, T.; Hachtel, W.
Curr. Genet. 23, 265-270, 1993
A:Title: In-frame length mutations associated with short tandem repeats are located in u
A:Reference number: S29795; MUID:93169690; PMID:8435856
A:Accession: S29795
A:Molecule type: DNA
A:Residues: 1-721 <NIM>
A:Cross-references: UNIPROT:P31568; EMBL:X64616; NID:g14334; PID:g14335
C:Genetics:
A:Genome: chloroplast
C:Keywords: Chloroplast

Query Match 21.6%; Score 114.5; DB 2; Length 721;
Best Local Similarity 28.8%; Pred. No. 7.4;
Matches 36; Conservative 21; Mismatches 45; Indels 23; Gaps 4;

Qy 6 LELEKVLATLDP-----EGK-----TQDELQ--KEAAAEALNEKVEALQNVAALEEL 52
Db 170 LELEGALVGSSPTSEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEV 229
Qy 53 SKLEDNL-----KDAETNNVEDYIKEGLEEAIAATKKAELEKTKQKELDAAALNELGP 102
Db 230 EGTEEEVGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEG 289

Qy 103 DGDEE 107
Db 290 TEDEE 294

RESULT 10
A59234
slow myosin heavy chain 3 - quail
C:Species: Coturnix coturnix
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59234
R:Nikovic Jr., W.; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, L.; Stock
J. Biol. Chem. 271, 17047-17056, 1996
A:Title: Isolation and characterization of an avian slow myosin heavy chain gene express
A:Reference number: A59234; MUID:96291845; PMID:8663323
A:Accession: A59234
A:Status: Preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-1931 <NIK>
A:Cross-references: GB:U53862; NID:g1289513; PIDN:AAC59912.1; PID:g1289514
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:81-761/Domain: myosin motor domain homology <MWO>

Query Match 21.6%; Score 114.5; DB 2; Length 1931;
Best Local Similarity 34.4%; Pred. No. 20;
Matches 43; Conservative 19; Mismatches 36; Indels 27; Gaps 7;

Qy 1 LEDAELEKVLATL-----DPEGKTODE-----LDKEAAAEALNEKVEALQNOV 45
Db 1002 LDDQAEEDKNTVLAKKVKLEQQADDESLSLOQEKIRMDLERAKRKLEGGDLKLAESV 1061
Qy 46 AELEELSKLEDNL--KDAETNNVEDYIKEGLEEAIAATKKAELEKTKQKELDAAALNELGPD 103
Db 1062 MDLENDQQLLEERLKKDFELNTLNARIED--EQAIA--AQLQKLELQARTEEL--- 1113
Qy 104 GDDEE 108
Db 1114 --EEE 1116

RESULT 11
148153
myosin heavy chain beta, cardiac muscle [similarity] - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148153; A28298
R:Wang, R.; Sole, M.J.; Cukerman, E.; Liew, C.C.
J. Mol. Cell. Cardiol. 26, 1155-1165, 1994
A:Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chai
A:Reference number: 148153; MUID:95115033; PMID:7815459
A:Accession: 148153
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1934 <RES>
A:Cross-references: UNIPROT:P13540; GB:L12104; NID:g402371; PIDN:AAA62313.1; PID:g402372
R:Jandreski, M.A.; Sole, M.J.; Liew, C.C.
Nucleic Acids Res. 16, 4737, 1988
A:Title: Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain.
A:Reference number: A28298; MUID:88247788; PMID:330703
A:Accession: A28298
A:Molecule type: mRNA
A:Residues: 962-965, 'E', 967-980, 'E', 981-985, 'Q', 987-1007, 'A', 1009, 'E', 1011, 'RKT', 1015-10
536, 'L', 1538-1555, 'K', 1557-1934 <JAN>
A:Cross-references: GB:X07273; NID:G49640; PIDN:CAA30256.1; PID:G49641
A:Note: the authors translated the codon GTG for residue 1504 as Leu
C:Genetics:
A:Introns: 66/3; 114/3; 167/1; 176/2; 212/3; 243/3; 265/1; 298/1; 322/3; 379/1; 418/3; 4
23/3; 1389/2; 1450/3; 1506/1; 1547/3; 1650/3; 1718/3; 1760/3; 1852/3; 1884/3; 1929/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; muscle; nucleotide b
F:87-765/Domain: myosin motor domain homology <MMOT>
F:177-184/Region: nucleotide-binding motif A (P-loop)

Query Match 21.6%; Score 114.5; DB 2; Length 1934;
Best Local Similarity 33.0%; Pred. No. 20;
Matches 38; Conservative 21; Mismatches 43; Indels 13; Gaps 4;

Qy 7 ELEKVLATLDPD-GKTODELDK-EAAAEALNEKVEALQNVAALEELSKLEDNLKDAET 64
Db 843 ETEKEMATKEEFGVRVDALKESEARRKELEEKVMSLQEKNDLQLOQVAPQDNLADAE 902
Qy 65 N-----NVEDYIKEGLE--EAIATKKAEELEKTKQKELDAAALNELGPDGDEE 108
Db 903 RCDQLKKNKIQLEAKVKEMTERLEDEEEMNAELTAKRKLEDECSSELKRDIDDLE 957

RESULT 12
I38055
myosin heavy chain, perinatal skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.4.1)

```

Qy      6  LELEKVLV---TLDPEGKTQDELDK-----AAEAELENEKVEALQNVAAEEELSKELEDN 58
Db      306 LEMERLVALPETPDNGKSGPESVTEVVVPSSENSLASETEVLTSTRTKELEEKLEKLE-- 363
Qy      59  LKDAETNNVEDYIKEGLEPEAI-----ATKAAELEKTQKELDAAELN 100
Db      364  ---AEKHELENEVKNEEAHVHIENSEVLTSTRTKELEEKLEKLEAKSEEL 411

RESULT 7
S07537
myosin heavy chain, smooth muscle, splice form 2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S07537; S10449
R:Baby, P.; Periaesamy, M.
J. Mol. Biol. 210, 673-679, 1989
A:Title: Myosin heavy chain isoform diversity in smooth muscle is produced by
A:Reference number: S07537; MUID:90133920; PMID:2614841

```

Query Match 21.7%; Score 115; DB 2; Length 412;
Best Local Similarity 33.9%; Pred. No. 4;
Matches 43; Conservative 16; Mismatches 42; Indels 26; Gaps 5

```

Qy   2  EDAEAELEKVLATLDPEGKTQDELDKGAAEAELNEKVLAQNQVALEBEL-----S2
      |||:|||::||::||::||::||::||::||::||::||::||::||::||
Db   33  EDAKLRLEVNMQAL-----KGQFERDLOARDEQNEEKRRQLQRQLHVEYTELEDERKQRAL 88
      |||:|||::||::||::||::||::||::||::||::||::||::||
Qy   53  -----SKEDNLNKAETNNVSDYIKEGLEAIAITKK---AELEKTOKELD---AALNELG 101
      |||:|||::||::||::||::||::||::||::||::||::||::||
Db   89  AAAAKKUEGGDKULELO--ADSAVKGREEAIKOLRKLQAOMKDFORELDDARASRDEIF 146
      |||:|||::||::||::||::||::||::||::||::||::||::||
Qy   102 PDGDEEE 108
       |||
Db   147 ATSKENE 153

```

RESULT 8
S10450
myosin heavy chain, smooth muscle, splice form 1 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date : 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10450; S07827
R;BabuJ, P.; Periaasamy, M.
submitted to the EMBL Data Library, August 1989
A;Reference number: S10449
A;Accession: S10450
A;Molecule type: mRNA
A;Residues: 1-621 <BAB>
A;Cross-references: UNIPROT:Q63339; EMBL:X16262; NID:G56650; PIDN:CAA34348.1;
A;Experimental source: Sprague-Dawley; smooth muscle; clone RAMHC21

J. Mol. Biol. 210, 673-679, 1989
K;Basilj, F.; Periasamy, M.
A;Title: Myosin heavy chain isoform diversity in smooth muscle is produced by differential
A;Reference number: S07537
A;Reference number: MUID:90133920; PMID:2614841

A:Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:AE007317; PIDN:AAK98925.1; PID:gl
C:Genetics: pspA
A:Gene: pspA
Query Match 38.9%; Score 206; DB 2; Length 619;
Best Local Similarity 46.4%; Pred. No. 2.6e-05;
Matches 51; Conservative 17; Mismatches 24; Indels 18; Gaps 3;
Qy 7 ELEKVLATLDPEGKTQDELK-----AAEALNEKVEALQNQVALEEE 50
Db 211 ELENQVHRLEQLEKIDSESDYAKGFRAPLQSKLDKAKKLS-KLEELSDKIDELDA 269
Qy 51 ELSKLEDNLKDA-ETNNVEDYIKEGLEAIAATKKALEKTKQKELDAALNE 99
Db 270 ETAKLEDQLKAAEENNVEDYFKEGLEKTIAAKKALEKTEADLKAYNE 319
RESULT 3
A1971
surface protein pspA precursor - Streptococcus pneumoniae
N:Alternate names: pneumococcal surface protein A
C:Species: Streptococcus pneumoniae
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A41971; A60282; A33134
R:Yother, J.; Briles, D.E.
J. Bacteriol. 174, 601-609, 1992
A:Title: Structural properties and evolutionary relationships of PspA, a surface protein
A:Reference number: A41971; MUID:92105030; PMID:1729249
A:Accession: A41971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-619 <YOT>
A:Cross-references: UNIPROT:Q54972; UNIPROT:Q8DR10; GB:M74122; NID:gl53840; PIDN:AAA2701
A:Note: sequence extracted from NCBI backbone (NCBI:75635, NCBI:75636)
R:Talington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.E.
Infect. Immun. 59, 1285-1289, 1991
A:Title: A 43-kilodalton pneumococcal surface protein, PspA: isolation, protective ability
A:Reference number: A60282; MUID:91169598; PMID:2004810
A:Accession: A60282
A:Molecule type: protein
A:Residues: 32-76 <TAL>
A:Experimental source: strain JV2008
C:Genetics: pspA
A:Gene: pspA
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-619/Product: surface protein pspA #status predicted <MAT>
F:411-430/Domain: cpl repeat homology <CP01>
F:431-450/Domain: cpl repeat homology <CP02>
F:451-470/Domain: cpl repeat homology <CP03>
F:471-490/Domain: cpl repeat homology <CP04>
F:491-510/Domain: cpl repeat homology <CP05>
F:511-530/Domain: cpl repeat homology <CP06>
F:531-550/Domain: cpl repeat homology <CP07>
F:551-570/Domain: cpl repeat homology <CP08>
F:571-591/Domain: cpl repeat homology <CP09>
F:592-611/Domain: cpl repeat homology <CP10>
Query Match 38.9%; Score 206; DB 2; Length 619;
Best Local Similarity 46.4%; Pred. No. 2.6e-05;
Matches 51; Conservative 17; Mismatches 24; Indels 18; Gaps 3;
Qy 7 ELEKVLATLDPEGKTQDELK-----AAEALNEKVEALQNQVALEEE 50
Db 211 ELENQVHRLEQLEKIDSESDYAKGFRAPLQSKLDKAKKLS-KLEELSDKIDELDA 269
Qy 51 ELSKLEDNLKDA-ETNNVEDYIKEGLEAIAATKKALEKTKQKELDAALNE 99
Db 270 ETAKLEDQLKAAEENNVEDYFKEGLEKTIAAKKALEKTEADLKAYNE 319
RESULT 4
S03166
myosin heavy chain, gizzard smooth muscle [similarity] - chicken

N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S03166; A27066; A26045; A36604; A43298
R:Yanagisawa, M.; Hamada, Y.; Katsuragawa, Y.; Imamura, M.; Mikawa, T.; Masaki, T.
J. Mol. Biol. 198, 143-157, 1987
A:Title: Complete primary structure of vertebrate smooth muscle myosin heavy chain deduced from complementary DNA
A:Reference number: S03166; MUID:88118918; PMID:2892941
A:Accession: S03166
A:Molecule type: mRNA
A:Residues: 1-1979 <YAN>
A:Cross-references: UNIPROT:P10587; EMBL:X06546; NID:g63633; PIDN:CAA29793.1; PID:g63634
A:Note: part of this sequence was confirmed by protein sequencing
R:Malta, T.; Onishi, H.; Yajima, E.; Matsuda, G.
J. Biochem. 102, 133-145, 1987
A:Title: Amino acid sequence of the amino-terminal 24 kDa fragment of the heavy chain of
A:Reference number: A27066; MUID:98032919; PMID:3312184
A:Accession: A27066
A:Molecule type: protein
A:Residues: 2, 'Z', 4-204 <MAI>
R:Onishi, H.; Malta, T.; Miyanishi, T.; Watanabe, S.; Matsuda, G.
J. Biochem. 100, 1433-1447, 1986
A:Title: Amino acid sequence of the 203-residue fragment of the heavy chain of chicken gizzard smooth muscle myosin
A:Reference number: A26045; MUID:87194651; PMID:3571180
A:Accession: A26045
A:Molecule type: protein
A:Residues: 653-855 <ONI>
R:Onishi, H.; Malta, T.; Matsuda, G.; Fujiwara, K.
J. Biol. Chem. 265, 19362-19368, 1990
A:Title: Lys-65 and Glu-168 are the residues for carbodiimide-catalyzed cross-linking between myosin heavy chain and actin
A:Reference number: A36604; MUID:91035476; PMID:1977747
A:Accession: A36604
A:Status: preliminary
A:Molecule type: protein
A:Residues: 54-67; 146-183 <ON2>
R:Cole, D.G.; Yount, R.G.
Biochemistry 31, 6186-6192, 1992
A:Title: Stability and photochemical properties of vanadate-trapped nucleotide complexes of myosin
A:Reference number: A43298; MUID:92329440; PMID:1385724
A:Accession: A43298
A:Status: preliminary
A:Molecule type: protein
A:Residues: 189-183 <COL>
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; blocked amino end; coiled coil; hydrolase; methylated amino end
F:87-777/Domain: myosin motor domain homology <MMOT>
F:177-184/Region: nucleotide-binding motif A (P-loop)
F:565-578/Region: actin binding #status predicted
F:639-653/Region: actin binding #status predicted
F:850-1940/Domain: coiled coil <COL>
F:850-1290/Region: S2
F:1291-1979/Region: light meromyosin
F:1941-1979/Domain: carboxyl-terminal <CBT>
F:2/Modified site: blocked amino end (Ser) (in mature form) #status experimental
F:128/Modified site: N6,N6-trimethyllysine (Lys) #status experimental
F:183/Binding site: ATP (Lys) #status predicted
F:707,717/Active site: Cys #status predicted
Query Match 22.1%; Score 117; DB 1; Length 1979;
Best Local Similarity 30.6%; Pred. No. 14;
Matches 38; Conservative 24; Mismatches 30; Indels 32; Gaps 5;
Qy 4 AELEKVLATLDPEGKTQDELK-----AAEALNEKVEALQNQVALEEEESKLEDN 58
Db 1043 SELEVR-----LKKEKSRQLEKIKRKGESDLHQIAELQAQIAELKAKKXEE 1097
Qy 59 LKDA-----ETNNVEDYIKE-----GLEAIAATKKALEKTK-----ELDAA 96
Db 1098 LQAALAELEDETSQNNALKKIRELSHISDLQEDLESEKAARNKAKQKRDLELEAL 1157
Qy 97 LNEL 100
Db 1158 KTEL 1161

| Result No. | Score | Query | | Length | DB | ID | Description |
|------------|-------|-------|------|--------|--------|--------------------|-------------|
| | | Match | % | | | | |
| 1 | 322 | 60.9 | 744 | 2 | F95013 | pneumococcal surfa | |
| 2 | 206 | 38.9 | 619 | 2 | A97887 | surface protein ps | |
| 3 | 206 | 38.9 | 619 | 2 | A41971 | surface protein ps | |
| 4 | 117 | 22.1 | 1979 | 1 | S03166 | myosin heavy chain | |
| 5 | 116 | 21.9 | 256 | 2 | S58923 | tropomyosin isofo | |
| 6 | 115.5 | 21.8 | 779 | 2 | C96805 | hypothetical prote | |
| 7 | 115 | 21.7 | 412 | 2 | S07537 | myosin heavy chain | |
| 8 | 115 | 21.7 | 621 | 2 | S10450 | myosin heavy chain | |
| 9 | 114.5 | 21.6 | 721 | 2 | S23795 | hypothetical prote | |
| 10 | 114.5 | 21.6 | 1931 | 2 | A59234 | slow myosin heavy | |
| 11 | 114.5 | 21.6 | 1934 | 2 | I48153 | myosin heavy chain | |
| 12 | 114.5 | 21.6 | 1937 | 2 | I38055 | myosin heavy chain | |
| 13 | 114 | 21.6 | 1938 | 2 | JC5421 | smooth muscle myo | |
| 14 | 114 | 21.6 | 1972 | 2 | JCS420 | smooth muscle myo | |
| 15 | 113.5 | 21.5 | 630 | 2 | S23796 | hypothetical prote | |
| 16 | 113.5 | 21.5 | 1509 | 1 | A27224 | myosin heavy chain | |
| 17 | 113.5 | 21.5 | 1940 | 1 | A24922 | myosin heavy chain | |
| 18 | 113.5 | 21.5 | 1940 | 1 | S04090 | myosin heavy chain | |
| 19 | 113.5 | 21.5 | 2139 | 2 | T18296 | myosin heavy chain | |
| 20 | 112.5 | 21.3 | 1961 | 1 | A61231 | myosin heavy chain | |
| 21 | 112 | 21.2 | 284 | 2 | A44980 | tropomyosin, obliq | |
| 22 | 112 | 21.2 | 284 | 2 | S58921 | tropomyosin, isofo | |
| 23 | 111.5 | 21.1 | 279 | 2 | D71453 | hypothetical prote | |
| 24 | 111.5 | 21.1 | 1177 | 2 | B75150 | chromosome segrega | |
| 25 | 111.5 | 21.1 | 1938 | 2 | I49464 | alpha cardiac myos | |
| 26 | 111.5 | 21.1 | 2354 | 2 | T14156 | kinesin-related pr | |
| 27 | 111 | 21.0 | 484 | 2 | B33501 | myosin heavy chain | |
| 28 | 111 | 21.0 | 1993 | 2 | T22661 | hypothetical prote | |
| 29 | 111 | 21.0 | 1972 | 1 | A41604 | myosin heavy chain | |

```

DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Bg7561.
XX
FH Key Location/Qualifiers
FT Misc-difference 44 /note= "unidentified amino acid"
XX
XX WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
XX (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
DR WPI; 1997-202002/18.
XX
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
XX in vaccines for protecting animals against S.pneumoniae infection.
PS Example 6; Fig 13; 296pp; English.
XX
CC This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7561.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 184 AA;
Query Match 70.2%; Score 371.5; DB 2; Length 184;
Best Local Similarity 76.0%; Pred. No. 4.6e-22;
Matches 79; Conservative 11; Mismatches 13; Indels 1; Gaps 1;
QY 5 ELELEKVLATLDPEGKTODELDKEAAEAELEKVEALONQVAELEEEELSKLEDNLKDAET 64
DB 4 KVNLENLLST-DPGKTDDELDKGAEEAELEKVKVALLPNVXELEELSPEDNLKDAET 62
QY 65 NNVEDYIKFLEAEATKAELEKTKQELDAALNELGPDGDEE 108
DB 63 NHVEDYIKFLEAEATKAELEETPQEVDAALNDLVPDGGEE 106

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Search completed: November 17, 2005, 20:19:43
Job time : 77.7468 secs

```
RESULT 13
ABW02622
ID ABW02622 standard; protein; 212 AA.
XX
AC ABW02622;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bg7817c pneumococcal surface protein A (PspA) central region.
XX
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX
OS Unidentified.
XX
PN US6592876-B1.
XX
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.
XX
DR Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX
PS Example 6; SEQ ID NO 68; 121pp; English.
XX
CC The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg7817c
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 212 AA;
Query Match 87.0%; Score 460; DB 7; Length 212;
Best Local Similarity 88.0%; Pred. No. 4.4e-29;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 LEDAELEKVLATLDPEKQTQDELDKAAAEALNKVEALQNQVAELEEEELSKLEDNLK 60
DB 28 LEKAGAGLNLSTLDPEKQTQDELDKAAAEALNKVEALPNQVAELEEEELSKLEDNLK 87
QY 61 DAETNNVEDYIIEGLEEAATKKALEKTKQELDAALNELGPDGDEEE 108
DB 88 DAETNNVEDYIIEGLEEAATKKALEKTKQELDAALNELGPDGDEEE 135
RESULT 14
ABW02623
ID ABW02623 standard; protein; 185 AA.
XX
AC ABW02623;
XX
DT 17-OCT-2003 (revised)
```

```
XX 12-FEB-2004 (first entry)
DT
XX Bg7561c pneumococcal surface protein A (PspA) central region.
DE
XX
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 45
FT /label= Unknown
XX
XX US6592876-B1.
XX
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.
XX
DR Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX
PS Example 6; SEQ ID NO 69; 121pp; English.
XX
CC The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg7561c
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 185 AA;
Query Match 74.7%; Score 395; DB 7; Length 185;
Best Local Similarity 77.9%; Pred. No. 6.1e-24;
Matches 81; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
QY 5 ELELEKVLATLDPEKQTQDELDKAAAEALNKVEALQNQVAELEEEELSKLEDNLKDAET 64
DB 4 KVNLENLSTLDPEKQTQDELDKAAAEALNKVEALPNVXLEEEELSPEDNLKDAET 63
QY 65 NNVEDYIIEGLEEAATKKALEKTKQELDAALNELGPDGDEEE 108
DB 64 NNVEDYIIEGLEEAATKKALEKTKQELDAALNELGPDGDEEE 107
RESULT 15
AAW14589
ID AAW14589 standard; protein; 184 AA.
XX
AC AAW14589;
XX
DT 17-OCT-2003 (revised)
```


CC used in the exemplification of the invention

XX Sequence 211 AA;

Query Match 91.3%; Score 483; DB 7; Length 211;

Best Local Similarity 90.7%; Pred. No. 6.4e-31;

Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNOVAEEELSLEDNLK 60

Db 25 LEKAAELENLLSTLDPEGKTQDELDEKAAAEALNEKVEALPNQVSELEELSLEDNLK 84

Qy 61 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 108

Db 85 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 132

RESULT 11

AAW14587

ID AAW14587 standard; protein; 238 AA.

XX AC AAW14587;

XX DT 17-OCT-2003 (revised)

XX DT 28-OCT-1997 (first entry)

XX DE Streptococcus pneumoniae PspA central region.

XX KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;

XX KW bacteraemia; pneumonia.

XX OS Streptococcus pneumoniae; strain Bg11703.

XX PN WO9709994-A1.

XX PD 20-MAR-1997.

XX PF 16-SEP-1996; 96WO-US014819.

XX PR 15-SEP-1995; 95US-00529055.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

XX PI Hollingshead S, Tart R, Brooks-Walter A;

XX DR WPI; 1997-202002/18.

XX PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used

XX PT in vaccines for protecting animals against S.pneumoniae infection.

XX PS Example 6; Fig 13; 296pp; English.

XX CC This sequence shows the central portion, including the C-terminus of the

XX CC alpha-helix region and some of the proline-rich region, of pneumococcal

XX CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg11703.

XX CC Comparison of the N-terminal and central regions (AAW14533-57 and

XX CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can

XX CC be used to divide the strains into several families based on sequence

XX CC homologies. PspA polypeptides, or fragments of them, can be used in

XX CC vaccines to protect animals against S. pneumoniae infection and hence for

XX CC the prevention of diseases such as otitis media, meningitis, bacteraemia

XX CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical

XX CC region and the immediate 5' tip of the coding sequence are likely to be

XX CC the critical sequences for predicting PspA cross-reactions and vaccine

XX CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 238 AA;

Query Match

Best Local Similarity 91.3%; Score 483; DB 2; Length 238;

Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNOVAEEELSLEDNLK 60

Db 28 LEKAAELENLLSTLDPEGKTQDELDEKAAAEALNEKVEALPNQVSELEELSLEDNLK 87

Qy 61 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 108

Db 88 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 135

Query Match

Best Local Similarity 90.7%; Pred. No. 7.3e-31;

Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNOVAEEELSLEDNLK 60

Db 28 LEKAAELENLLSTLDPEGKTQDELDEKAAAEALNEKVEALPNQVSELEELSLEDNLK 87

Qy 61 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 108

Db 88 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 135

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNOVAEEELSLEDNLK 60

Db 25 LEKAAELENLLSTLDPEGKTQDELDEKAAAEALNEKVEALPNQVSELEELSLEDNLK 84

Qy 61 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 108

Db 85 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 132

RESULT 12

AAW14588

ID AAW14588 standard; protein; 212 AA.

XX AC AAW14588;

XX DT 17-OCT-2003 (revised)

XX DT 28-OCT-1997 (first entry)

XX DE Streptococcus pneumoniae PspA central region.

XX KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;

XX KW KW bacteraemia; pneumonia.

XX OS Streptococcus pneumoniae; strain Bg7817.

XX PN WO9709994-A1.

XX PD 20-MAR-1997.

XX PF 16-SEP-1996; 96WO-US014819.

XX PR 15-SEP-1995; 95US-00529055.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

XX PI Hollingshead S, Tart R, Brooks-Walter A;

XX DR WPI; 1997-202002/18.

XX PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used

XX PT in vaccines for protecting animals against S.pneumoniae infection.

XX PS Example 6; Fig 13; 296pp; English.

XX CC This sequence shows the central portion, including the C-terminus of the

XX CC alpha-helix region and some of the proline-rich region, of pneumococcal

XX CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7817.

XX CC Comparison of the N-terminal and central regions (AAW14533-57 and

XX CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can

XX CC be used to divide the strains into several families based on sequence

XX CC homologies. PspA polypeptides, or fragments of them, can be used in

XX CC vaccines to protect animals against S. pneumoniae infection and hence for

XX CC the prevention of diseases such as otitis media, meningitis, bacteraemia

XX CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical

XX CC region and the immediate 5' tip of the coding sequence are likely to be

XX CC the critical sequences for predicting PspA cross-reactions and vaccine

XX CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 212 AA;

Query Match

Best Local Similarity 87.0%; Score 460; DB 2; Length 212;

Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNOVAEEELSLEDNLK 60

Db 28 LEKAAELENLLSTLDPEGKTQDELDEKAAAEALNEKVEALPNQVSELEELSLEDNLK 87

Qy 61 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 108

Db 88 DAETNNVEDYIKGLEEAIATKKAELKTKQELDAALNELGPDGDEEE 135

PT Isolated PspC amino acid sequence used as polymerase chain reaction or
PT hybridization probe, comprises pneumococcal surface protein having alpha-
PT helical, proline rich and repeat regions.
XX
PS Disclosure; Col 145-188; 186pp; English.
XX
CC The present invention relates to the isolation of Streptococcus
CC pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide
CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-
CC like protein having alpha-helical, proline rich and repeat regions. The
CC PspC and PspA proteins may be used in a vaccine to protect against
CC pneumococcal infections. The polynucleotide sequences encoding PspC and
CC PspA may be used for the expression of the proteins, and as PCR primers
CC or hybridization probes. The present sequence represents S. pneumoniae
CC PspA protein
XX
SQ Sequence 8991 AA;

Query Match 100.0%; Score 529; DB 6; Length 8991;
Best Local Similarity 100.0%; Pred. NO. 8.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEEELSLEDNLK 60
DB 8615 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEEELSLEDNLK 8674

QY 61 DAETNNVEDYIKEGLEEAIAATKKAELKTKQKELDAALNELGPDGDEE 108
DB 8675 DAETNNVEDYIKEGLEEAIAATKKAELKTKQKELDAALNELGPDGDEE 8722

RESULT 9
AAW14590
ID AAW14590 standard; protein; 233 AA.
XX
AC AAW14590;
XX
DT 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Ef5668.
XX
XX WO9709994-A1.
PN
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
DR
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
PS Example 6; Fig 13; 296pp; English.
XX
CC This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Ef5668 (see
CC also AAW14592). Comparison of the N-terminal and central regions
CC (AAW14533-57 and AAW14562-91) of PspA from different pneumococcal strains
CC can be used to divide the strains into several families based on sequence

CC homologues. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 233 AA;

Query Match 98.0%; Score 518.5; DB 2; Length 233;
Best Local Similarity 99.1%; Pred. NO. 1e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEEELSLEDNL 59
DB 51 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNOVAEEELSLEDNL 110

QY 60 KDAETNNVEDYIKEGLEEAIAATKKAELKTKQKELDAALNELGPDGDEE 108
DB 111 KDAETNNVEDYIKEGLEEAIAATKKAELKTKQKELDAALNELGPDGDEE 159

RESULT 10
ABW02621
ID ABW02621 standard; protein; 211 AA.
XX
AC ABW02621;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bg11703c pneumococcal surface protein A (PspA) central region.
XX
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX
OS Unidentified.
XX
PN US6592876-B1.
XX
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
PI
XX WPI; 2003-862841/80.
DR
XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX
PS Example 6; SEQ ID NO 67; 121pp; English.
XX
CC The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg11703c
CC pneumococcal surface protein A (PspA) central region. This sequence is

PF 17-FEB-2003; 2003WO-US008199.
 XX
 PR 15-MAR-2002; 2002US-0365351P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Briles DE;
 XX
 XX WPI; 2004-192068/18.
 XX
 DR Treating Streptococcus pneumoniae infection in a subject lacking a
 PT functional spleen comprises administering an antibody that recognizes
 PT pneumococcal surface protein A (PspA) or its binding portion.
 XX
 PS Claim 17; SEQ ID NO 1; 41pp; English.
 XX
 XX The present invention relates to treating Streptococcus pneumoniae
 CC infection in a subject lacking a functional spleen comprises
 CC administering an antibody that recognizes pneumococcal surface protein A
 CC (PspA) or its binding portion. The method is useful for treating or
 CC preventing Streptococcus pneumoniae infection in a subject lacking a
 CC functional spleen. The disease-associated injury is especially due to
 CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
 CC anemia or Hodgkin's disease. The present sequence represents PspA
 CC molecule from the Rxi strain of Streptococcus pneumoniae.
 XX
 SQ Sequence 653 AA;
 Query Match 100.0%; Score 529; DB 8; Length 653;
 Best Local Similarity 100.0%; Pred. No. 4.7e-34;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVVAEELEELSLEDNLK 60
 Db 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVVAEELEELSLEDNLK 335
 Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELGPDGDEE 108
 Db 336 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELGPDGDEE 383
 RESULT 7
 ADO52080
 ID ADO52080 standard; protein; 653 AA.
 AC ADO52080;
 XX
 XX 12-AUG-2004 (first entry)
 DT
 DE S. pneumoniae strain EF5688 PspA protein.
 XX
 XX Immunogenic composition; vaccine; Th2-type immune response;
 KW pneumococcal surface protein A; PspA.
 XX
 OS Streptococcus pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= Signal_peptide
 FT Protein 32..653
 FT /note= "S. pneumoniae strain EF5688 mature PspA protein"
 FT Domain 110..384
 FT /note = PspA alpha-helical domain
 XX
 XX US2004101531-A1.
 PN
 XX 27-MAY-2004.
 PD
 XX 15-APR-2003; 2003US-00414532.
 PF
 XX 16-APR-2002; 2002US-0372710P.
 PR
 XX (CURT/) CURTISS R.
 PA

PA (KANG/) KANG H Y.
 XX
 PI Curtiss R, Kang HY;
 XX
 DR WPI; 2004-399655/37.
 DR N-PSDB; ADO52067.
 XX
 PT New vaccine comprising a live attenuated strain of pathogenic gram-
 PT negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 PT or bacteria.
 XX
 XX Example 5; SEQ ID NO 26; 94pp; English.
 PS
 XX The invention relates to immunogenic compositions and vaccines comprising
 CC a live attenuated strain of pathogenic gram negative bacteria that
 CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
 CC response in a vertebrate against pathogens, e.g., helminths, fungi,
 CC viruses, protozoans or bacteria. The present sequence is Streptococcus
 CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA). This
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 653 AA;
 Query Match 100.0%; Score 529; DB 8; Length 653;
 Best Local Similarity 100.0%; Pred. No. 4.7e-34;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVVAEELEELSLEDNLK 60
 Db 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNEKVEALQNVVAEELEELSLEDNLK 335
 Qy 61 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELGPDGDEE 108
 Db 336 DAETNNVEDYIKGLEEAIATKKALEKTKQELDAALNELGPDGDEE 383
 RESULT 8
 ABU08487
 ID ABU08487 standard; protein; 8991 AA.
 XX
 AC ABU08487;
 XX
 XX 24-JUN-2003 (first entry)
 DT
 DE S. pneumoniae pneumococcal surface protein A (PspA) protein.
 XX
 XX Pneumococcal surface protein C; PspC; pneumococcal surface protein A;
 KW alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;
 KW antibacterial.
 XX
 OS Streptococcus pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..8991
 FT /note= "All Xaa residues within this sequence are
 FT unknown"
 XX
 XX US6500613-B1.
 PN
 XX 31-DEC-2002.
 PD
 XX 16-SEP-1996; 96US-00714741.
 PF
 XX 15-SEP-1995; 95US-00529055.
 PR
 XX (UYAL-) UNIV ALABAMA.
 PA
 XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 XX
 XX WPI; 2003-361534/34.
 DR
 XX

XX 17-OCT-2003 (revised)
DT 27-OCT-1997 (first entry)
XX
XX Streptococcus pneumoniae PspA surface protein.
XX
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
XX Streptococcus pneumoniae; strain Ef5668.
OS
XX WO9709994-A1.
PN
XX 20-MAR-1997.
PD
XX
XX 16-SEP-1996; 96WO-US014819.
PF
XX
XX 15-SEP-1995; 95US-00529055.
PR
XX (UABR-) UAB RES FOUND.
PA
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
DR N-PSDB; AAT61724.
XX
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
XX Disclosure; Fig 13; 296pp; English.
XX
XX This sequence comprises the pneumococcal surface protein A (pspA) of
CC Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the
CC pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be
CC used in vaccines to protect animals against S. pneumoniae infection and
CC hence for the prevention of diseases such as otitis media, meningitis,
CC bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 458 AA;
SQ
Query Match 100.0%; Score 529; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.2e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 60
DB 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 335
QY 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
DB 336 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 383
RESULT 5
ABW02626
ID ABW02626 standard; protein; 458 AA.
XX
XX ABW02626;
AC
XX
DT 12-FEB-2004 (first entry)
XX
DE Ef5668 pneumococcal surface protein A (PspA).
XX
XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
KW
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 458
FT /note= "Encoded by GC"

XX US6592876-B1.
PN
XX 15-JUL-2003.
PD
XX
XX 15-SEP-1995; 95US-00529055.
PF
XX
XX 20-APR-1993; 93US-00048896.
PR
XX 06-JUN-1995; 95US-00465746.
PR
XX (UABR-) UAB RES FOUND.
PA
XX
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
PI
XX WPI; 2003-862841/80.
DR N-PSDB; AAD64535.
XX
XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX
XX Example 6; SEQ ID NO 73; 121pp; English.
XX
XX The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Ef5668 pneumococcal
CC surface protein A (PspA) used in the exemplification of the invention
XX
XX Sequence 458 AA;
SQ
Query Match 100.0%; Score 529; DB 7; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.2e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 60
DB 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVAALEEEELSKLEDNLK 335
QY 61 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 108
DB 336 DAETNNVEDYIKEGLEEAATKKALEKTQKELDAALNELGPDGDEEE 383
RESULT 6
ADK52495
ID ADK52495 standard; protein; 653 AA.
XX
XX ADK52495;
AC
XX
DT 20-MAY-2004 (first entry)
XX
XX PspA molecule from the Rx1 strain of Streptococcus pneumoniae.
XX
XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
KW Hodgkin's disease.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO2004016231-A2.
PN
XX 26-FEB-2004.
PD
XX

CC vaccines and in gene therapy. The present sequence is EF5688
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 529; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 60
DB 51 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 110

QY 61 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 108
DB 111 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 158

RESULT 2
ADOS2055
ID ADOS2055 standard; protein; 275 AA.
XX
AC ADOS2055;
XX
DT 12-AUG-2004 (first entry)
XX
DE S. pneumoniae strain EF5688 PspA alpha helical domain.
XX
KW Immunogenic composition; vaccine; Th2-type immune response;
KW pneumococcal surface protein A; PspA.
XX
OS Streptococcus pneumoniae.
XX
PN US2004101531-A1.
XX
PD 27-MAY-2004.
XX
PF 15-APR-2003; 2003US-00414532.
XX
PR 16-APR-2002; 2002US-0372710P.
XX
PA (CURT/) CURTISS R.
PA (KANG/) KANG H Y.
XX
PI CurtiSS R, Kang HY;
XX
XX WPI; 2004-399655/37.
XX
PT New vaccine comprising a live attenuated strain of pathogenic gram-
PT negative bacteria, useful in eliciting a Th2-type immune response in a
PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
PT or bacteria.
XX
PS Claim 17; SEQ ID NO 1; 94pp; English.
XX
XX The invention relates to immunogenic compositions and vaccines comprising
CC a live attenuated strain of pathogenic gram negative bacteria that
CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
CC response in a vertebrate against pathogens, e.g., helminths, fungi,
CC viruses, protozoans or bacteria. The present sequence is Streptococcus
CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
CC helical domain. This sequence is used in the invention.
XX
SQ Sequence 275 AA;

Query Match 100.0%; Score 529; DB 8; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 60
DB 167 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 226

QY 61 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 108
DB 227 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 274

RESULT 3
ADK52496
ID ADK52496 standard; protein; 369 AA.
XX
AC ADK52496;
XX
DT 20-MAY-2004 (first entry)
XX
DE alpha helical region PspA molecule from the Rx1 strain.
XX
KW Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
KW Hodgkin's disease.
XX
OS Streptococcus pneumoniae.
XX
PN WO2004016231-A2.
XX
PD 26-FEB-2004.
XX
PF 17-FEB-2003; 2003WO-US008199.
XX
PR 15-MAR-2002; 2002US-0365351P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE;
XX
DR WPI; 2004-192068/18.
XX
PT Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX
PS Claim 17; SEQ ID NO 2; 41pp; English.
XX
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rx1 strain of Streptococcus
CC pneumoniae.
XX
SQ Sequence 369 AA;

Query Match 100.0%; Score 529; DB 8; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 60
DB 245 LEDAELEKVLATLDPEGKTQDELDKAAAEALNEKVEALQNVVAEEELSLEDNLK 304

QY 61 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 108
DB 305 DAETNNVEDYIKGEEAIAIKKAELEKTKQELDAALNELGPDGDEE 352

RESULT 4
AAW14592
ID AAW14592 standard; protein; 458 AA.
XX
AC AAW14592;

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 76.7468 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-25
Perfect score: 529
Sequence: 1 LEDAELEKVLATLDPEK.....TQKELDAALNELGPDGDEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query % | Length | DB | ID | Description |
|------------|-------|-------|---------|--------|----------|----------|-------------|
| 1 | 529 | 100.0 | 232 | 7 | ABW02624 | Abw02624 | Ef5668c p |
| 2 | 529 | 100.0 | 275 | 8 | ADO52055 | Ado52055 | S. pneumo |
| 3 | 529 | 100.0 | 369 | 8 | ADK52496 | Adk52496 | alpha hel |
| 4 | 529 | 100.0 | 458 | 2 | AAW14592 | Aaw14592 | Streptoco |
| 5 | 529 | 100.0 | 458 | 7 | ABW02826 | Abw02826 | Ef5668 pn |
| 6 | 529 | 100.0 | 653 | 8 | ADK52495 | Adk52495 | PspA mole |
| 7 | 529 | 100.0 | 653 | 8 | ADO52080 | Ado52080 | S. pneumo |
| 8 | 529 | 100.0 | 8991 | 6 | ABU08487 | Abu08487 | S. pneumo |
| 9 | 518.5 | 98.0 | 233 | 2 | AAW14590 | Aaw14590 | Streptoco |
| 10 | 483 | 91.3 | 211 | 7 | ABW02621 | Abw02621 | Bg11703c |
| 11 | 483 | 91.3 | 238 | 2 | AAW14587 | Aaw14587 | Streptoco |
| 12 | 460 | 87.0 | 212 | 2 | AAW14588 | Aaw14588 | Streptoco |
| 13 | 460 | 87.0 | 212 | 7 | ABW02622 | Abw02622 | Bg7817c p |
| 14 | 395 | 74.7 | 185 | 7 | ABW02623 | Abw02623 | Bg7561c p |
| 15 | 371.5 | 70.2 | 184 | 2 | AAW14589 | Aaw14589 | Streptoco |
| 16 | 361.5 | 68.3 | 459 | 8 | ADO15316 | Ado15316 | S. pneumon |
| 17 | 322.5 | 61.0 | 487 | 8 | ADRO4321 | Adro4321 | Streptoco |
| 18 | 322.5 | 61.0 | 489 | 8 | ADO52088 | Ado52088 | Streptoco |
| 19 | 322.5 | 61.0 | 527 | 8 | ADO52082 | Ado52082 | E. coli B |
| 20 | 322.5 | 61.0 | 624 | 8 | ADO52129 | Ado52129 | E. coli B |
| 21 | 322 | 60.9 | 416 | 8 | ADK52498 | Adk52498 | alpha hel |
| 22 | 322 | 60.9 | 526 | 8 | ADK52497 | Adk52497 | PspA mole |
| 23 | 322 | 60.9 | 744 | 6 | ABU00449 | Abu00449 | S. pneumo |
| 24 | 322 | 60.9 | 744 | 8 | ADM92054 | Adm92054 | S. pneumon |
| 25 | 322 | 60.9 | 745 | 3 | AAW81652 | Aaw81652 | Streptoco |

ALIGNMENTS

RESULT 1
ABW02624
ID ABW02624 standard; protein; 232 AA.
XX AC ABW02624;
XX AC
DT 12-FEB-2004 (first entry)
XX DE Ef5668c pneumococcal surface protein A (PspA) central region.
XX DE
XX KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX OS Unidentified.
XX OS
XX PN US5592876-B1.
XX PN
XX PD 15-JUL-2003.
XX PD
XX PF 15-SEP-1995; 95US-00529055.
XX PF
XX PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX (UABR-) UAB RES FOUND.
XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
WPI; 2003-862841/80.
Immunological composition for obtaining expression products used for detecting the presence of Streptococcus pneumoniae or its strain, comprises at least two different full length isolated gene encoding pneumococcal surface protein A.
Example 6; SEQ ID NO 70; 121pp; English.
The present invention relates to an immunological composition comprising at least 2 different full length isolated genes encoding pneumococcal surface protein A (PspAs) from different groups based on restriction fragment polymorphism analysis. The invention is useful for obtaining expression products by recombinant techniques to detect, determine, isolate or diagnose the presence of Streptococcus pneumoniae or its strain. The expression product is useful for preparing antigenic, immunological or vaccine compositions, for eliciting antibodies, an immunological response (other than or additional to antibodies), or a protective response (including antibody or other immunological response by administering compositions to a host). The invention is also useful as

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; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa at position 2 is unknown
US-10-299-636-62

Query Match 59.0%; Score 317; DB 15; Length 213;
Best Local Similarity 65.7%; Pred. No. 2.1e-17;
Matches 71; Conservative 9; Mismatches 24; Indels 4; Gaps 2;
QY 1 LEKAGAGLENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVAEEELSLEDNLK 60
Db 59 LAKQTELEKLLDNLDPGKTQDELDKAAAEALNKKVEALPNQVADELEKISNLEILLG 118
QY 61 DAETHNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
Db 119 GADP---ED-DTAALPNKLTAKKAEFEKTPKELDAALNELGPDGDEEE 162

RESULT 14
US-10-674-755-21
; Sequence 21, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-21

Query Match 58.3%; Score 313; DB 15; Length 104;
Best Local Similarity 65.7%; Pred. No. 1.9e-17;
Matches 71; Conservative 9; Mismatches 24; Indels 4; Gaps 2;
QY 1 LEKAGAGLENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVAEEELSLEDNLK 60
Db 1 LAKQTELEKLLDNLDPGKTQDELDKAAAEALNKKVEALPNQVADELEKISNLEILLG 60
QY 61 DAETHNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
Db 61 GADP---ED-DTAALPNKLTAKKAELEKTPKELDAALNELGPDGDEEE 104

RESULT 15
US-10-674-755-20
; Sequence 20, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-20
Query Match 57.9%; Score 311; DB 15; Length 104;
Best Local Similarity 64.8%; Pred. No. 2.7e-17;
Matches 70; Conservative 11; Mismatches 23; Indels 4; Gaps 2;
QY 1 LEKAGAGLENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVAEEELSLEDNLK 60
Db 1 LAKQTELEKLLDNLDPGKTQDELDKAAAEALNKKVEALPNQVADELEKISNLEILLG 60
QY 61 DAETHNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
Db 61 GADS---ED-DTAALPNKLTAKKAELEKTPKELDAALNELGPDGDEEE 104
Search completed: November 17, 2005, 20:29:18
Job time : 71.832 secs

Qy 1 LEKAGAGLENLLSTLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 60
 Db 276 LEDAELEKVLATLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 335

Qy 61 DAETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 336 DAETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 383

RESULT 10
 US-10-414-532-26
 ; Sequence 26, Application US/10414532
 ; Publication No. US20040101531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTISS III, ROY
 ; APPLICANT: KANG, HO YOUNG
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
 ; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
 ; FILE REFERENCE: 56029-40437
 ; CURRENT APPLICATION NUMBER: US/10/414,532
 ; CURRENT FILING DATE: 2003-04-15
 ; PRIOR APPLICATION NUMBER: 60/372,710
 ; PRIOR FILING DATE: 2002-04-16
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 26
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-10-414-532-26

Query Match 87.0%; Score 467; DB 16; Length 653;
 Best Local Similarity 88.9%; Pred. No. 1e-28;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLLSTLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 60
 Db 276 LEDAELEKVLATLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 335

Qy 61 DAETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 336 DAETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 383

RESULT 11
 US-10-674-755-26
 ; Sequence 26, Application US/10674755
 ; Publication No. US20040067237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BECKER et al.
 ; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
 ; FILE REFERENCE: 454312-2471
 ; CURRENT APPLICATION NUMBER: US/10/674,755
 ; CURRENT FILING DATE: 2003-09-30
 ; PRIOR APPLICATION NUMBER: US/09/147,875A
 ; PRIOR FILING DATE: 1999-05-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 26
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (1)..(108)
 ; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
 US-10-674-755-26

Query Match 84.5%; Score 454; DB 15; Length 108;
 Best Local Similarity 87.0%; Pred. No. 1.4e-28;
 Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLLSTLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 60

Db 1 LEKAAELENLLSTLDPGGKTQDELKGAABAEALNKKVEALPNVXLEEBLSPPEDNLK 60
 Qy 61 DAETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 61 DAETHNHVEDYIKGLEEAIATKQAELEETPOEVDAAALNDLVPDGGEE 108

RESULT 12
 US-10-299-636-84
 ; Sequence 84, Application US/10299636
 ; Publication No. US20040077847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briles, David E
 ; APPLICANT: McDaniel, Larry S
 ; APPLICANT: Swiatlo, Edwin
 ; APPLICANT: Yother, Janet
 ; APPLICANT: Crain, Marilyn J
 ; APPLICANT: Hollingshead, Susan
 ; APPLICANT: Tart, Rebecca
 ; APPLICANT: Brooks-Walter, Alexis
 ; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 57909/361
 ; CURRENT APPLICATION NUMBER: US/10/299,636
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: 08/714,741
 ; PRIOR FILING DATE: 1996-09-16
 ; PRIOR APPLICATION NUMBER: 08/529,055
 ; PRIOR FILING DATE: 1995-09-15
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 84
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (45)
 ; OTHER INFORMATION: Xaa at position 45 is unknown
 US-10-299-636-84

Query Match 81.8%; Score 439; DB 15; Length 185;
 Best Local Similarity 84.1%; Pred. No. 3.9e-27;
 Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 EKAGAGLENLLSTLDPGGKTQDELKGAABAEALNKKVEALPNQVAELEEBLSKLEDNLK 61
 Db 1 KKQVNLNLLSTLDPGGKTQDELKGAABAEALNKKVEALPNVXLEEBLSPPEDNLK 60

Qy 62 AETHNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 61 AETHNHVEDYIKGLEEAIATKQAELEETPOEVDAAALNDLVPDGGEE 107

RESULT 13
 US-10-299-636-62
 ; Sequence 62, Application US/10299636
 ; Publication No. US20040077847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briles, David E
 ; APPLICANT: McDaniel, Larry S
 ; APPLICANT: Swiatlo, Edwin
 ; APPLICANT: Yother, Janet
 ; APPLICANT: Crain, Marilyn J
 ; APPLICANT: Hollingshead, Susan
 ; APPLICANT: Tart, Rebecca
 ; APPLICANT: Brooks-Walter, Alexis
 ; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 57909/361
 ; CURRENT APPLICATION NUMBER: US/10/299,636
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: 08/714,741
 ; PRIOR FILING DATE: 1996-09-16

Db 60 DAETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106

RESULT 6

US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-25

Query Match 87.0%; Score 467; DB 15; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.3e-29;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LEKAGAGLENLSTLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 60

Db 1 LEDAELEKVLATLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 60

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 7

US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-85

Query Match 87.0%; Score 467; DB 15; Length 232;
Best Local Similarity 88.9%; Pred. No. 3.1e-29;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LEKAGAGLENLSTLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 60

Db 51 LEDAELEKVLATLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 110

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 111 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 158

RESULT 8

US-10-414-532-1
; Sequence 1, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-1

Query Match 87.0%; Score 467; DB 16; Length 275;
Best Local Similarity 88.9%; Pred. No. 3.8e-29;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LEKAGAGLENLSTLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 60

Db 167 LEDAELEKVLATLDPEGKTODELDKEAAEALNKKEALPNOVAEEELSLEDNLK 226

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 227 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 274

RESULT 9

US-10-299-636-88
; Sequence 88, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-88

Query Match 87.0%; Score 467; DB 15; Length 458;
Best Local Similarity 88.9%; Pred. No. 6.8e-29;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

```
US-10-299-636-83
; Sequence 83, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-83

Query Match          98.7%; Score 530; DB 15; Length 212;
Best Local Similarity 99.1%; Pred. No. 2.9e-34;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVAEELEELSKELDNLK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 28 LEKAGAGLENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVAEELEELSKELDNLK 87
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-10-674-755-23
; Sequence 23, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-23

Query Match          95.2%; Score 511; DB 15; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.2e-33;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVAEELEELSKELDNLK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 LEKAAEAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVSELEELSKELDNLK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

US-10-299-636-82
; Sequence 82, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-82

Query Match          95.2%; Score 511; DB 15; Length 211;
Best Local Similarity 96.3%; Pred. No. 9.1e-33;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVAEELEELSKELDNLK 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 LEKAAEAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVSELEELSKELDNLK 84
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Qy 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 132
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RESULT 5
US-10-674-755-22
; Sequence 22, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-22

Query Match          90.9%; Score 488; DB 15; Length 106;
Best Local Similarity 96.3%; Pred. No. 2.7e-31;
Matches 104; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOVAEELEELSKELDNLK 60
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Db 1 LEKAAEAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNOV-ELEELSKELDNLK 59
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Qy 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 71.932 Seconds
(without alignments)
629.082 Million cell updates/sec

Title: US-10-674-755-24
Perfect score: 537
Sequence: 1 LEKAGAGLENLLTLDPEGK.....TPKELDAALNELGPDGDEE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 537 | 100.0 | 108 | 15 | US-10-674-755-24 |
| 2 | 530 | 98.7 | 212 | 15 | US-10-299-636-83 |
| 3 | 511 | 95.2 | 108 | 15 | US-10-674-755-23 |
| 4 | 511 | 95.2 | 211 | 15 | US-10-299-636-82 |
| 5 | 488 | 90.9 | 106 | 15 | US-10-674-755-22 |
| 6 | 467 | 87.0 | 108 | 15 | US-10-674-755-25 |
| 7 | 467 | 87.0 | 232 | 15 | US-10-299-636-85 |
| 8 | 467 | 87.0 | 275 | 16 | US-10-414-532-1 |
| 9 | 467 | 87.0 | 458 | 15 | US-10-299-636-88 |
| 10 | 467 | 87.0 | 653 | 16 | US-10-414-532-26 |
| 11 | 454 | 84.5 | 108 | 15 | US-10-674-755-26 |

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| 12 | 439 | 81.8 | 185 | 15 | US-10-299-636-84 | Sequence 84, Appl |
| 13 | 317 | 59.0 | 213 | 15 | US-10-299-636-62 | Sequence 62, Appl |
| 14 | 313 | 58.3 | 104 | 15 | US-10-674-755-21 | Sequence 21, Appl |
| 15 | 311 | 57.9 | 104 | 15 | US-10-674-755-20 | Sequence 20, Appl |
| 16 | 306.5 | 57.1 | 459 | 16 | US-10-702-305A-18 | Sequence 18, Appl |
| 17 | 306 | 57.0 | 744 | 10 | US-09-769-787-184 | Sequence 184, App |
| 18 | 306 | 57.0 | 744 | 17 | US-10-472-928-32 | Sequence 32, Appl |
| 19 | 305 | 56.8 | 641 | 9 | US-09-765-272-160 | Sequence 160, App |
| 20 | 305 | 56.8 | 641 | 20 | US-11-106-649-160 | Sequence 59, Appl |
| 21 | 300 | 55.9 | 197 | 15 | US-10-299-636-59 | Sequence 67, Appl |
| 22 | 295 | 54.9 | 233 | 15 | US-10-299-636-67 | Sequence 18, Appl |
| 23 | 290 | 54.0 | 102 | 15 | US-10-674-755-18 | Sequence 27, Appl |
| 24 | 287.5 | 53.5 | 119 | 15 | US-10-674-755-27 | Sequence 58, Appl |
| 25 | 287.5 | 53.5 | 215 | 15 | US-10-299-636-58 | Sequence 34, Appl |
| 26 | 272 | 50.7 | 487 | 16 | US-10-414-532-34 | Sequence 21, Appl |
| 27 | 272 | 50.7 | 487 | 16 | US-10-414-532-21 | Sequence 28, Appl |
| 28 | 272 | 50.7 | 524 | 16 | US-10-414-532-28 | Sequence 65, Appl |
| 29 | 262.5 | 48.9 | 290 | 16 | US-10-414-532-65 | Sequence 32, Appl |
| 30 | 261 | 48.6 | 230 | 16 | US-10-414-532-32 | Sequence 19, Appl |
| 31 | 261 | 48.6 | 230 | 16 | US-10-414-533-19 | Sequence 19, Appl |
| 32 | 235 | 43.8 | 80 | 15 | US-10-674-755-19 | Sequence 19, Appl |
| 33 | 197 | 36.7 | 354 | 15 | US-10-299-636-105 | Sequence 105, App |
| 34 | 197 | 36.7 | 588 | 15 | US-10-299-636-96 | Sequence 96, Appl |
| 35 | 197 | 36.7 | 619 | 10 | US-09-882-774-1 | Sequence 1, Appl |
| 36 | 197 | 36.7 | 619 | 15 | US-10-282-122A-73702 | Sequence 73702, A |
| 37 | 197 | 36.7 | 619 | 16 | US-10-414-532-72 | Sequence 72, Appl |
| 38 | 192 | 35.8 | 204 | 15 | US-10-299-636-66 | Sequence 66, Appl |
| 39 | 188 | 35.0 | 99 | 15 | US-10-674-755-11 | Sequence 11, Appl |
| 40 | 184.5 | 34.4 | 100 | 15 | US-10-674-755-12 | Sequence 12, Appl |
| 41 | 183 | 34.1 | 198 | 15 | US-10-299-636-76 | Sequence 76, Appl |
| 42 | 169 | 31.5 | 141 | 14 | US-10-254-995-2 | Sequence 2, Appl |
| 43 | 169 | 31.5 | 195 | 15 | US-10-299-636-86 | Sequence 86, Appl |
| 44 | 169 | 31.5 | 589 | 9 | US-09-748-875-14 | Sequence 14, Appl |
| 45 | 169 | 31.5 | 589 | 10 | US-09-298-523B-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-674-755-24
; Sequence 24, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-24

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| Query Match | 100.0% | Score 537; | DB 15; | Length 108; |
| Best Local Similarity | 100.0%; | Pred. No. 3.7e-35; | | |
| Matches 108; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | LEKAGAGLENLLTLDPEGKTQDELKKAALNKKVEALPNQVALEEEELSKLEDNLK | 60 | |
| Db | 1 | LEKAGAGLENLLTLDPEGKTQDELKKAALNKKVEALPNQVALEEEELSKLEDNLK | 60 | |
| Qy | 61 | DAETNHVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE | 108 | |
| Db | 61 | DAETNHVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE | 108 | |
| RESULT 2 | | | | |

; CLASSIFICATION: 435

RESULT 8

RESULT 10

RESULT 9

Query Match 87.0%; Score 467; DB 2; Length 108;
Best Local Similarity 88.9%; Pred. No. 2.6e-35;

Query Match 95.2%; Score 511; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.7e-39;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;


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; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-68

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Best Local Similarity 99.1%; Pred. No. 1.1e-40;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEKAGAGLNLSTLDPEGKTQDELKAEAAELNKKVEALPNQVAEEBELSKLEDNLK 60
Db 28 LEKAGAGLNLSTLDPEGKTQDELKAEAAELNKKVEALPNQVAEEBELSKLEDNLK 87

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Db 88 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELPGDGDDEE 135

RESULT 3
US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996

; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-68

Query Match      98.7%; Score 530; DB 4; Length 212;
Best Local Similarity 99.1%; Pred. No. 1.1e-40;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELPGDGDDEE 108
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RESULT 3
US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996

; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match      98.7%; Score 530; DB 4; Length 8991;
Best Local Similarity 99.1%; Pred. No. 1e-38;
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Db 8255 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELPGDGDDEE 8302

RESULT 4
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-22
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: November 17, 2005, 18:59:20 ; Search time 20.7935 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-24
Perfect score: 537
Sequence: 1 LEKAGAGLENTLTDPEGK.....TPKELDAALNELPGDDEEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------|-------------------|
| 1 | 537 | 100.0 | 108 | US-09-147-875A-24 | Sequence 24, Appl |
| 2 | 530 | 98.7 | 212 | US-08-529-055-68 | Sequence 68, Appl |
| 3 | 530 | 98.7 | 8991 | US-08-714-741-32 | Sequence 32, Appl |
| 4 | 527 | 98.1 | 108 | US-08-710-749-22 | Sequence 22, Appl |
| 5 | 527 | 98.1 | 108 | US-08-710-749-23 | Sequence 23, Appl |
| 6 | 511 | 95.2 | 108 | US-08-710-749-26 | Sequence 26, Appl |
| 7 | 511 | 95.2 | 108 | US-09-147-875A-23 | Sequence 23, Appl |
| 8 | 511 | 95.2 | 211 | US-08-529-055-67 | Sequence 67, Appl |
| 9 | 488 | 90.9 | 106 | US-09-147-875A-22 | Sequence 22, Appl |
| 10 | 467 | 87.0 | 108 | US-08-710-749-24 | Sequence 24, Appl |
| 11 | 467 | 87.0 | 108 | US-09-147-875A-25 | Sequence 25, Appl |
| 12 | 467 | 87.0 | 232 | US-08-529-055-70 | Sequence 70, Appl |
| 13 | 467 | 87.0 | 458 | US-08-529-055-73 | Sequence 73, Appl |
| 14 | 454 | 84.5 | 108 | US-08-710-749-25 | Sequence 25, Appl |
| 15 | 454 | 84.5 | 108 | US-09-147-875A-26 | Sequence 26, Appl |
| 16 | 439 | 81.8 | 185 | US-08-529-055-69 | Sequence 69, Appl |
| 17 | 321 | 59.8 | 104 | US-08-710-749-20 | Sequence 20, Appl |
| 18 | 317 | 59.0 | 213 | US-08-529-055-47 | Sequence 47, Appl |
| 19 | 313 | 58.3 | 104 | US-09-147-875A-21 | Sequence 21, Appl |
| 20 | 311 | 57.9 | 104 | US-08-710-749-19 | Sequence 19, Appl |
| 21 | 311 | 57.9 | 104 | US-09-147-875A-20 | Sequence 20, Appl |
| 22 | 305 | 56.8 | 641 | US-08-961-083-160 | Sequence 160, App |
| 23 | 305 | 56.8 | 641 | US-09-536-784-160 | Sequence 160, App |
| 24 | 300 | 55.9 | 197 | US-08-529-055-44 | Sequence 44, Appl |
| 25 | 295 | 54.9 | 233 | US-08-529-055-52 | Sequence 52, Appl |
| 26 | 290 | 54.0 | 102 | US-08-710-749-21 | Sequence 21, Appl |
| 27 | 290 | 54.0 | 102 | US-09-147-875A-18 | Sequence 18, Appl |

ALIGNMENTS

RESULT 1

US-09-147-875A-24
; Sequence 24, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-24

Query Match 100.0%; Score 537; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|----|---|-----|
| Qy | 1 | LEKAGAGLENTLTDPEGKTQDELKAEAEALNKVVEALPNQVAEELEESKLEDNLK | 60 |
| Db | 1 | LEKAGAGLENTLTDPEGKTQDELKAEAEALNKVVEALPNQVAEELEESKLEDNLK | 60 |
| Qy | 61 | DAETNHVEDYIKGLEEAIAIKQAELEKTPKELDAALNELPGDDEEE | 108 |
| Db | 61 | DAETNHVEDYIKGLEEAIAIKQAELEKTPKELDAALNELPGDDEEE | 108 |

RESULT 2

US-08-529-055-68
; Sequence 68, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York

Db 19 LAKQTGLEKLLDSLDPEGKTODELDKEAAEALDKADELQNKVADLEKEISNLEILLG 78

Qy 61 DAETNHVEDYIKEGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 79 GADP---ED-DTAAIQNKLAITTKAELEKTQKELDAALNELGPDGDEEE 122

Search completed: November 17, 2005, 20:37:53

Job time : 65.0187 secs

| | | |
|---|---|--|
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | |
| OC | Streptococcus. | |
| OX | NCBI_TaxID=1313; | |
| QY | [1] | |
| RN | SEQUENCE FROM N.A. | |
| RP | RC STRAIN=69; | |
| RC | MEDLINE=20472698; PubMed=11015380; | |
| RX | RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.; | |
| RA | RT "Pneumococcal pspA sequence types of prevalent multiresistant | |
| RT | RT pneumococcal strains in the United States and of internationally | |
| RT | disseminated clones."; | |
| RL | J. Clin. Microbiol. 38:3663-3669(2000). | |
| QY | [2] | |
| RN | SEQUENCE FROM N.A. | |
| RP | RC STRAIN=69; | |
| RC | RA Beall B.W.; | |
| RA | RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AF255508; AAF70098.1; -. | |
| FT | NON_TER 1 1 | |
| FT | NON_TER 242 242 | |
| SQ | SEQUENCE 242 AA; 25843 MW; 707EA930797D2C82 CRC64; | |
| Query Match 60.1%; Score 323; DB 2; Length 242; | | |
| Best Local Similarity 67.6%; Pred. No. 3.8e-12; | | |
| Matches 73; Conservative 11; Mismatches 20; Indels 4; Gaps 2; | | |
| QY | 1 LEKAGAGLEMLLSTLDPGKGTQDELKDKEAAEALNKKVEALPNOVALEBEELSKELDNKLK 60 | |
| DB | 70 LAKQTELEKLLDLSLDPGKGTQDELKDKEAAEALNKKVEALQNKVADLEKEISNLEILG 129 | |
| QY | 61 DARTNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108 | |
| DB | 130 GADS--ED-DTAAQLQNKLATKKAELKTKQELDAALNELGPDGDEE 173 | |
| RESULT 15 | | |
| QY4593 | PRELIMINARY; PRT; 209 AA. | |
| ID | Q9L593 | |
| AC | Q9L593; | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) | |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) | |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | |
| DE | PspA (Fragment). | |
| GN | Name=pspA; | |
| OS | Streptococcus pneumoniae. | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | |
| OC | Streptococcus. | |
| OX | NCBI_TaxID=1313; | |
| QY | [1] | |
| RN | SEQUENCE FROM N.A. | |
| RP | RC STRAIN=115; | |
| RC | MEDLINE=20472698; PubMed=11015380; | |
| RX | RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.; | |
| RA | RT "Pneumococcal pspA sequence types of prevalent multiresistant | |
| RT | RT pneumococcal strains in the United States and of internationally | |
| RT | disseminated clones."; | |
| RL | J. Clin. Microbiol. 38:3663-3669(2000). | |
| QY | [2] | |
| RN | SEQUENCE FROM N.A. | |
| RP | RC STRAIN=115; | |
| RC | RA Beall B.W.; | |
| RA | RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AF254256; AAF68091.1; -. | |
| FT | NON_TER 1 1 | |
| FT | NON_TER 209 209 | |
| SQ | SEQUENCE 209 AA; 22628 MW; 06FF588F7C3B587 CRC64; | |
| Query Match 57.9%; Score 311; DB 2; Length 209; | | |
| Best Local Similarity 64.8%; Pred. No. 1.7e-11; | | |
| Matches 70; Conservative 11; Mismatches 23; Indels 4; Gaps 2; | | |
| QY | 1 LEKAGAGLEMLLSTLDPGKGTQDELKDKEAAEALNKKVEALPNOVALEBEELSKELDNKLK 60 | |
| DB | 70 LAKQTELEKLLDLSLDPGKGTQDELKDKEAAEALNKKVEALQNKVADLEKEISNLEILG 129 | |

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OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254255; AAF68090.1; -.
FT NON_TER 1
FT NON_TER 257
SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 65.8%; Score 353.5; DB 2; Length 257;
Best Local Similarity 63.9%; Pred. No. 5.9e-14;
Matches 76; Conservative 13; Mismatches 19; Indels 11; Gaps 2;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNOVALEBELSKLE 56
Db 51 LEKAEAELENLSTLDPEGKTQDELDEKAAEDANTEALQNKVADLENKVAELDKVETRLQ 110

Qy 57 DNLKDAETNHVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEE 108
Db 111 SDLKDAEENNVEDYIKEGLEKALTDKKVELNNTOKALDTAQAALDTALNELGPDGDEE 169

RESULT 10
Q9LAX6 PRELIMINARY; PRT; 461 AA.
AC Q9LAX6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6303;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071820; AAF27715.1; -.
FT NON_TER 461
FT NON_TER 461
SQ SEQUENCE 461 AA; 51563 MW; 249435F65585BB92 CRC64;

Query Match 63.0%; Score 338.5; DB 2; Length 461;
Best Local Similarity 60.5%; Pred. No. 8.5e-13;
Matches 72; Conservative 15; Mismatches 21; Indels 11; Gaps 2;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNOVALEBELSKLE 56
Db 273 LEDAELEKVLATLDPEGKTQDELDEKAAEDANTEALQNKVADLENKVAELDKVETRLQ 332

Qy 57 DNLKDAETNHVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEE 108
Db 333 SDLKDAEENNVEDYIKEGLEKALTDKKVELNNTOKALDTAQAALDTALNELGPDGDEE 391

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RESULT 11
Q9LS95 PRELIMINARY; PRT; 256 AA.
AC Q9LS95;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254254; AAF68089.1; -.
FT NON_TER 1
FT NON_TER 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match 61.5%; Score 330.5; DB 2; Length 256;
Best Local Similarity 59.7%; Pred. No. 1.4e-12;
Matches 71; Conservative 15; Mismatches 22; Indels 11; Gaps 2;

Qy 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNOVALEBELSKLE 56
Db 52 LEDAELEKVLATLDPEGKTQDELDEKAAEDANTEALQNKVADLENKVAELDKVETRLQ 111

Qy 57 DNLKDAETNHVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEE 108
Db 112 SDLKDAEENNVEDYIKEGLEKALTDKKVELNNTOKALDTAQAALDTALNELGPDGDEE 170

RESULT 12
Q9KGS0 PRELIMINARY; PRT; 227 AA.
AC Q9KGS0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA protein (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RA Beall B.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288751; AAF91495.1; -.

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EMBL: U89711; AAC62252.1; -.
HSP; P06653; IHX
InterPro: IPR002479; CW binding.
InterPro: IPR002345; Lipocalin.
InterPro: IPR009053; Prefoldin.
Pfam: PF01473; CW binding 1; 9.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN 1.
SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

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|------------|------------|--|-------|-------------|----|--------|--------|------|
| Query | Mac2cn | 87.0%; | Score | 467; | DB | 2 | Length | 653; |
| Best Local | Similarity | 88.9%; | Pred. | No. 2.3-20; | | | | |
| Matches | 96; | Conservative | 5; | Mismatches | 7; | Indels | 0; | Gaps |
| QY | 1 | LEKAGAGLENLSTLDPEGTQDDELDEKAAEALNKKEVALPNQVAEELEELSLEDNLK | 60 | | | | | |
| | | : : | | | | | | |
| Db | 276 | LEDAEAELEKVLATLDPEGTQDDELDEKAAEALNKKEVALONQVAEELEELSLEDNLK | 335 | | | | | |
| QY | 61 | DAETNHVDEYIKGLEEEAIATKQAELEKTPKPELDAAALNELGPDDEEE | 108 | | | | | |
| Db | 336 | DAETNHVDEYIKGLEEAIATKKALEKTKOKELDAALNELGPDDEEE | 393 | | | | | |

| |
|---|
| SEQUENCE FROM N.A. |
| RC STRAIN=SP95; |
| RX MEDLINE=22241996; PubMed=12354862; |
| RA Dicuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A., |
| RA Lorino G., Recchia S., Pantosti A., Beall B.; |
| RA "Genotypes of invasive pneumococcal isolates recently recovered from |
| RT Italian patients."; |
| RL J. Clin. Microbiol. 40:3660-3665(2002). |
| DR ENBL; AF490265; AA37733.1; -. |
| FR NON_TER 1 1 |
| DT NON_TER 211 211 |
| SO SEQUENCE 211 AA: 23207 MW: 096BFBE0B8CD6483 CRC64: |

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Query Match      65.8%; Score 353.5; DB 2; Length 211;
Best Local Similarity 63.9%; Pred. No. 4.9e-14;
Matches 76; Conservative 13; Mismatches 19; Indels 11; Gaps 2;

Qy    1 LEKAGAGLENLLSTLDPEGTQDELKEAAE-----AELNKKVEALPNQVALEEEELS KLE 56
      ||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    5 LEXAEALENLLSTLDPEGTQDELKEAAEDVNIIEALQNKVADLENKNVAELDKVTRLQ 64
      ||||| :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy    57 DNLKDAAETHNVVDYIKEGLEEATATQAEELEKT-----PKELDAAINELGPDGDSEE 108
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    65 SDLKDAAENNVDDYVXEGUEKALTDDKKVELNNLTQKALDTAQAKLDTALNELGPDGDSEE 123
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
Q9LS94 PRELIMINARY; PRT; 257 AA.
ID Q9LS94 AC Q9LS94;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PspA (Fragment).
DE Name=pspA;
GN Streptococcus pneumoniae.
OC Bacteria: Firmicutes: Actinobactiales: Streptococcaceae:

```

| RESULT 4 | | | | | | | | | |
|--|--|---|------|---------|--|--|--|--|--|
| ID | Q8KQK2 | PRELIMINARY; | PRT; | 107 AA. | | | | | |
| Q8KQK2 | Q8KQK2 | | | | | | | | |
| DT | 01-OCT-2002 | (TrEMBLrel. 22, Created) | | | | | | | |
| DT | 01-OCT-2002 | (TrEMBLrel. 22, Last sequence update) | | | | | | | |
| DT | 01-OCT-2002 | (TrEMBLrel. 22, Last annotation update) | | | | | | | |
| DE | Pneumococcal surface protein A (Fragment). | | | | | | | | |
| GN | Name=pspA; | | | | | | | | |
| OS | Streptococcus pneumoniae. | | | | | | | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | | | | | | |
| OC | Streptococcus. | | | | | | | | |
| OX | NCBI_TaxID=1313; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=255/00; | | | | | | | | |
| RX | MEDLINE=22170754; PubMed=12183557; | | | | | | | | |
| RX | DOI=10.1128/JAI.70.9.5086-5090.2002; | | | | | | | | |
| RA | Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C., | | | | | | | | |
| RA | Dias W.O., Leite L.C.C.; | | | | | | | | |
| RT | Analysis of serum cross-reactivity and cross-protection elicited by | | | | | | | | |
| RT | immunization with DNA vaccines against Streptococcus pneumoniae | | | | | | | | |
| RT | expressing PspA fragments from different clades.; | | | | | | | | |
| RL | Infect. Immun. 70:5086-5090(2002). | | | | | | | | |
| DR | EMBL; AY082390; AAL92495.1; -. | | | | | | | | |
| FT | NON TER 1 | | | | | | | | |
| FT | NON TER 107 | | | | | | | | |
| FT | NON TER 107 AA; 11897 MW; 47913E25EB47D5CC CRC64; | | | | | | | | |
| SEQ | SEQUENCE | | | | | | | | |
| Query Match 91.1%; Score 489; DB 2; Length 107; | | | | | | | | | |
| Best Local Similarity 94.4%; Pred. No. 1.8e-22; | | | | | | | | | |
| Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | LEKAGAGLENLSTLDPEGKTODELDKEAAAEALNKVKVEALPNQVAEEELSKEEDNLK 60 | | | | | | | |
| DB | 1 | LEKAEAELENLSTLDPEGKTODELDKEAAAEALNKVKVEALQNVAELEELSKEEDNLK 60 | | | | | | | |
| QY | 61 | DAETNHVEDYIKEGLEEAATKQAELEKTPKELDAALNELGPDGDEE 107 | | | | | | | |
| DB | 61 | DAETNNVEDYIKEGLEEAATKKALEKTKQELDAALNELGPDGDEE 107 | | | | | | | |
| RESULT 5 | | | | | | | | | |
| ID | Q9LAX3 | PRELIMINARY; | PRT; | 480 AA. | | | | | |
| Q9LAX3 | Q9LAX3 | | | | | | | | |
| DT | 01-OCT-2000 | (TrEMBLrel. 15, Created) | | | | | | | |
| DT | 01-OCT-2000 | (TrEMBLrel. 15, Last sequence update) | | | | | | | |
| DT | 01-OCT-2003 | (TrEMBLrel. 25, Last annotation update) | | | | | | | |
| DE | PspA (Fragment). | | | | | | | | |
| GN | Name=pspA; | | | | | | | | |
| OS | Streptococcus pneumoniae. | | | | | | | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | | | | | | |
| OC | Streptococcus. | | | | | | | | |
| OX | NCBI_TaxID=1313; | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=BG7561; | | | | | | | | |
| RX | MEDLINE=20448953; PubMed=10992499; | | | | | | | | |
| RX | DOI=10.1128/JAI.68.10.5889-5900.2000; | | | | | | | | |
| RA | Hollingshead S.K., Becker R., Briles D.E.; | | | | | | | | |
| RT | "Diversity of pspA: mosaic genes and evidence for past recombination | | | | | | | | |
| RT | in Streptococcus pneumoniae.;" | | | | | | | | |
| RL | Infect. Immun. 68:5889-5900(2000). | | | | | | | | |
| DR | EMBL; AF071824; AAF27718.1; -. | | | | | | | | |
| DR</ | | | | | | | | | |

| Result No. | Score | Query % | | | DB | ID | Description |
|------------|-------|---------|--------|---|--------|---------------------|-------------|
| | | Match | Length | | | | |
| 1 | 498 | 92.7 | 479 | 2 | Q9LAX2 | Q9Lax2 streptococc | |
| 2 | 498 | 92.7 | 481 | 2 | Q9LAX5 | Q9Lax5 streptococc | |
| 3 | 494 | 92.0 | 246 | 2 | Q9L5B4 | Q9L5B4 streptococc | |
| 4 | 489 | 91.1 | 107 | 2 | Q8KQK2 | Q8Kqk2 streptococc | |
| 5 | 473 | 88.1 | 480 | 2 | Q9LAX3 | Q9Lax3 streptococc | |
| 6 | 467 | 87.0 | 213 | 2 | Q8GNS7 | Q8gns7 streptococc | |
| 7 | 467 | 87.0 | 653 | 2 | Q34097 | Q34097 streptococc | |
| 8 | 353.5 | 65.8 | 211 | 2 | Q8GNT0 | Q8gnt0 streptococc | |
| 9 | 353.5 | 65.8 | 257 | 2 | Q9L594 | Q9L594 streptococc | |
| 10 | 338.5 | 63.0 | 461 | 2 | Q9LAX6 | Q9Lax6 streptococc | |
| 11 | 330.5 | 61.5 | 256 | 2 | Q9L595 | Q9L595 streptococc | |
| 12 | 327.5 | 61.0 | 227 | 2 | Q9LXG0 | Q9Lxgs0 streptococc | |
| 13 | 325 | 60.5 | 222 | 2 | Q9L584 | Q9L584 streptococc | |
| 14 | 323 | 60.1 | 242 | 2 | Q9L562 | Q9L562 streptococc | |
| 15 | 311 | 57.9 | 209 | 2 | Q9L593 | Q9L593 streptococc | |
| 16 | 308 | 57.4 | 231 | 2 | Q9L579 | Q9L579 streptococc | |
| 17 | 308 | 57.4 | 241 | 2 | Q9L580 | Q9L580 streptococc | |
| 18 | 306 | 57.0 | 228 | 2 | Q9L5B8 | Q9L5b8 streptococc | |
| 19 | 306 | 57.0 | 235 | 2 | Q9L582 | Q9L582 streptococc | |
| 20 | 306 | 57.0 | 249 | 2 | Q9L5D4 | Q9L5d4 streptococc | |
| 21 | 306 | 57.0 | 252 | 2 | Q9L583 | Q9L583 streptococc | |
| 22 | 306 | 57.0 | 360 | 2 | Q8KQK3 | Q8Kqk3 streptococc | |
| 23 | 306 | 57.0 | 429 | 2 | Q9LAX7 | Q9Lax7 streptococc | |
| 24 | 306 | 57.0 | 526 | 2 | Q9LAX9 | Q9Lax9 streptococc | |
| 25 | 306 | 57.0 | 608 | 2 | Q8VQ55 | Q8vg55 streptococc | |
| 26 | 306 | 57.0 | 744 | 2 | Q97T39 | Q97t39 streptococc | |
| 27 | 304 | 56.6 | 249 | 2 | Q9L5B7 | Q9L5b7 streptococc | |
| 28 | 304 | 56.6 | 502 | 2 | Q9LAX8 | Q9Lax8 streptococc | |
| 29 | 303 | 56.4 | 249 | 2 | Q9L585 | Q9L585 streptococc | |
| 30 | 303 | 56.4 | 256 | 2 | Q9L590 | Q9L590 streptococc | |
| 31 | 205 | 38.2 | 417 | 2 | Q9LAX3 | Q9Lax3 streptococc | |

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Db 2103 ALANKQLELDKVNQYKELKKQYKRLAAAKDDDDSD 2139

RESULT 15

S35760

fcxA protein precursor - Streptococcus pyogenes

C:Species: Streptococcus pyogenes

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S35760; A42711

R:Podbielski, A.

submitted to the EMBL Data Library, November 1992

A:Reference number: S35760

A:Accession: S35760

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-415 <POD>

A:Cross-references: UNIPROT:Q54859; EMBL:X69324; NID:G311759; PIDN:CAA491650

R:Haanes, E.J.; Heath, D.G.; Cleary, P.P.

J. Bacteriol. 174, 4967-4976, 1992

A:Title: Architecture of the vir regulons of group A streptococci parallels

A:Reference number: A42711; MUID:92332431, PMID:11385809

A:Accession: A42711

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 343-415 <HAA>

A:Cross-references: GB:M86806; NID:g153630; PIDN:AAA26887.1; PID:g153631

A:Experimental source: strain CS101, OF+

A>Note: sequence extracted from NCHI backbone (NCBIN:108942, NCBI:P108945)

C:Superfamily: M5 protein

Query Match 19.4%; Score 104; DB 2; Length 415;

Best Local Similarity 32.7%; Pred. No. 8.7;

Matches 36; Conservative 14; Mismatches 52; Indels 8; Gaps

QY 1 LEKAGAGENLLSTLDP- GKTQDELKKEAAE-AELNKKVEALPNQVAELEEELSLEDN

Db 212 LOSEATLENLLGSAKHETLQAKLTDTATBAKAKLESQETTLNLLGSAKRELTDLQAK

QY 59 LKDAETNHVDYIKGLEEAATQAELEKTPKELDAALNELGPDGDEEE 108

Db 272 LDANAE-----KEKLSQAALKEKLEATKKELADLQAKLAATNQEKE 315

Search completed: November 17, 2005, 20:39:52

Job time : 15.1144 secs

A:Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e
A:Reference number: A59282; MUID:99077683; PMID:9858676
A:Accession: A59282
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1964 <BHA>
A:Cross-references: UNIPROT:Q93522; GB:AF055895; NID:g3660671; PIDN:AC03556.1; PID:g366
A:Experimental source: cell line XTC
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:84-764/Domain: myosin motor domain homology <MMO>

Query Match 20.2%; Score 108.5; DB 2; Length 1964;
Best Local Similarity 30.3%; Pred. No. 23;
Matches 30; Conservative 23; Mismatches 35; Indels 11; Gaps 3;

Qy 8 LENLSTLDPEGKTQDELKKAEEALNKKVEALPNQVAEELEELSKLED-----NLK 60
Db 1506 MEDLVSSKDDVGSVHELEK--SKALBQQAEMTKQLEELDELOATEDAKLRLEVNQ 1563

Qy 61 DAETHNVVEDYIKEGLEEAIAIKQAELEKTPKELDAALNE 99
Db 1564 AMKAQFERDL--QGRDEQSEDKKQLVRQVKEMEAELD 1600

RESULT 10
S23325
M2 protein precursor - Streptococcus pyogenes
A:Species: Streptococcus pyogenes
A:Variety: serotype M2
C:Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S23325; S35761; S61078; S60785
R:Bessen, D.E.; Fischetti, V.A.
Infest. Immun. 60, 124-135, 1992
A:Title: Nucleotide sequences of two adjacent M or M-like protein genes of group A strep
A:Reference number: S23325; MUID:92104662; PMID:1370269
A:Accession: S23325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <BES>
A:Cross-references: UNIPROT:P50468; EMBL:X61276; NID:g47369; PIDN:CAA43581.1; PID:g47370
R:Podbielski, A.
submitted to the EMBL Data Library, November 1992
A:Reference number: S35760
A:Accession: S35761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <POD>
A:Cross-references: EMBL:X69324
R:Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A:Description: Noncongruent relationships between variation in emml gene sequences and t
A:Reference number: S61072
A:Accession: S61078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 12-94 <WHA>
A:Cross-references: EMBL:U11958; NID:G533593; PIDN:AAA99574.1; PID:g1235820
R:Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A:Title: Non-congruent relationships between variation in emm gene sequences and the pop
A:Reference number: S60784; MUID:95198537; PMID:7891551
A:Accession: S60785
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 31-89 <WH2>
A:Cross-references: EMBL:U11958
C:Superfamily: M5 protein

Query Match 20.1%; Score 108; DB 2; Length 407;
Best Local Similarity 29.9%; Pred. No. 4.7;
Matches 35; Conservative 16; Mismatches 36; Indels 30; Gaps 3;

Qy 5 GAGLENLSTLDPEGKTQDELKKA--AAELNKKVEALPNQVAEELEELSKLEDNLKDA 62

Db 30 GAGFAN-QTTVKANSKNPVPVKKEAKLSEALHDKIKNLEEKAELEFKLDKVEEHKKV 88
Qy 63 ETNHVEDYIK-----EGLEEAIAIKQAELEKTPKE 92
Db 89 EEEHKDHEKLEKKSDEVERHYLRQLDQYKQEQQKRNLEELERQSQREVEKEKYQE 145

RESULT 11
C70445
ATPase subunit of ATP-dependent proteinase (EC 3.4.-.-) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: C70445
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70445
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1006 <AQF>
A:Cross-references: UNIPROT:O67588; GB:AE000750; NID:g2983999; PIDN:AA07550.1; PID:g298
A:Experimental source: strain VF5
C:Genetics:
A:Gene: clpB
C:Superfamily: endopeptidase Clp ATP-binding chain
C:Keywords: hydrolase

Query Match 19.9%; Score 107; DB 2; Length 1006;
Best Local Similarity 31.8%; Pred. No. 14;
Matches 34; Conservative 16; Mismatches 35; Indels 22; Gaps 4;

Qy 20 KTOBELDKAAEALNKKVEALPNQVAEELEELSKLEDNLKDAETHNVVEDYIKEG---LE 76
Db 522 KAITDALDQAAARKKL--KVGTPEIQEIERKIKALEEQI--ITANLKGDEKEAQLKIE 577

Qy 77 EA-----IATKQAELEKTPKELDAALNELGPDGDEEE 108
Db 578 KAKLEKEQELLGKVGVEAKIAELKKKIBELDEKIEKAAEKGDYK 624

RESULT 12
A59234
slow myosin heavy chain 3 - quail
C:Species: Coturnix coturnix
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59234
R:Nikovits Jr., W.; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, L.; Stock
J. Biol. Chem. 271, 17047-17056, 1996
A:Title: Isolation and characterization of an avian slow myosin heavy chain gene express
A:Reference number: A59234; MUID:96291845; PMID:8663323
A:Accession: A59234
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1931 <NIK>
A:Cross-references: GB:U53862; NID:g1289513; PIDN:AAC59912.1; PID:g1289514
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:81-761/Domain: myosin motor domain homology <MMO>

Query Match 19.9%; Score 107; DB 2; Length 1931;
Best Local Similarity 36.0%; Pred. No. 28;
Matches 41; Conservative 19; Mismatches 36; Indels 18; Gaps 6;

Qy 1 LEKAGAGLE---NLLSTLDPEGKTQDELKKAEEALNKKVEALPNQVAEELEELSKLE 56
Db 1015 LAKAKVLEQADDLSSLOQEKIR--MDLERAKRKLEGLDKLAQSVMDLENDKQOLE 1072

Qy 57 DNL--KDAETHNVVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEEE 108
Db 1073 ERUKKKDFELNTLNARIED--EQAIA---AQLQKKLQELQARIEEL-----EEE 1116

A>Title: Human nonmuscle myosin heavy chains are encoded by two genes located on different chromosomes

A:Reference number: A61231; MUID:9131803; PMID:1860190

A:Accession: A61231

A:Molecule type: mRNA

A:Residues: 1-715 <STM>

A:CROSS-references: UNIPROT:P35579; UNIPROT:Q9UMJ0; GB:M69180; NID:g189029; PIDN:AAA6176

R:Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990

A>Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alternative splicing

A:Reference number: A34876; MUID:90138958; PMID:1967836

A:Accession: A34876

A:Molecule type: mRNA

A:Residues: 715-1961 <SAB>

A:CROSS-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036

R:Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.; Blood 78, 1826-1833, 1991

A>Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, characterization of complementary DNA sequences

A:Reference number: 152562; MUID:92003925; PMID:1912569

A:Accession: 152562

A>Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: mRNA

A:Residues: 1-52, 'EAI', 56-659, 'T', 661-868, 'T', 870-930, 'C', 932-1239, 'KG', 1242-1337 <RES>

A:CROSS-references: GB:M1105; NID:g188988; PIDN:AAAS9888.1; PID:g553596

R:Bement, W.M.; Hasson, T.J.; With, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A>Title: Identification and overlapping expression of multiple unconventional myosin genes in rat skeletal muscle

A:Reference number: A55758; MUID:94294418; PMID:8022818

A:Accession: I61692

A>Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: mRNA

A:Residues: 182-218 <BEM>

A:CROSS-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134

C:Genetics:

A:Gene: GDB:MVH9

A:CROSS-references: GDB:I20216; OMIM:160775

A:Map position: 22q12.3-22q13.1

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide-binding site

F:84-764/Domain: myosin motor domain homology <MMOT>

F:174-181/Region: nucleotide-binding motif A (P-loop)

F:552-565/Region: actin binding #status predicted

F:628-640/Region: actin binding #status predicted

F:837-1938/Domain: coiled coil #status predicted <COI>

F:837-1277/Domain: S2 #status predicted <DS2>

F:1278-1961/Domain: light meromyosin #status predicted <LMM>

F:1939-1961/Domain: carboxyl-terminal <CBT>

F:125/Modified site: N6,N6-trimethyllysine (lys) #status predicted

F:180/Binding site: ATP (lys) #status predicted

F:694,704/Active site: Cys #status predicted

Query Match 20.6%; Score 110.5; DB 1; Length 1961;
Best Local Similarity 30.38; Pred. No. 17;
Matches 30; Conservative 24; Mismatches 34; Indels 11; Gaps 3;

Qy 8 LENLLSTLDPEGKTQDELDEKFAAEALNKVKVEALPNQVALEEEELSKLED-----NLK 60
:|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db 1507 MEDLMSSKDVGKSVHELEK--SKRALEQQVSEMKTKLEELEDQLATEDAKLRLENLQ 1564
:|::||::||::||::||::||::||::||::||::||::||::||::||:
Qy 61 DAETNHVEDYIKGLEFEAIAATKQAELEKTPKELDADINE 99
:|::||::||::||::||::||::||::||::||::||::||::||::||:
Db 1565 AMKAQFERDL--OGRDPSQEEKKKQLVRQVRMEAELED 1601
:|::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 7

A40997

myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)

N/Contains: myosin ATPase (EC 3.6.4.1)

C/Species: Aequipecten irradians

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A40997; S13557

R:Nyitrai, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.

J. Biol. Chem. 266, 18469-18476, 1991

A>Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Sec

A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:AE007317; PIDN:AAK98925.1; PID:gl
C;Genetics:
A;Gene: pspA

Query Match 36.7%; Score 197; DB 2; Length 619;
Best Local Similarity 45.0%; Pred. No. 1.6e-05;
Matches 50; Conservative 18; Mismatches 25; Indels 18; Gaps 3;

Qy 6 AGLENLLSTLDPEGKTQDELKQ-----AAAEALNKKVEALPNQVAELE 49
Db 210 AELENQVHRLEQELKEIDSESEYAKSGFRAPLQSKLDAAKKALS-KLEELSDKIDELD 268

Qy 50 BELSKLENLQDA-ETNHVEDYIKGLEBEATATQAELEKTPKELDAAINE 99

Db 269 AEIAKLEQLKAAEENNVEDYFKEGLEKTTAAKKAEELEKTEADLUKAVNE 319

RESULT 3

A41971

surface protein pspA precursor - Streptococcus pneumoniae

N;Alternate names: pneumococcal surface protein A

C;Species: Streptococcus pneumoniae

C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A41971; A60282; A33134

R;Yother, J.; Briles, D.E.

J. Bacteriol. 174, 601-609, 1992

A;Title: Structural properties and evolutionary relationships of PspA, a surface protein

A;Reference number: A41971; MUID:92105030; PMID:1729249

A;Accession: A41971

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-619 <YOT>

A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:M74122; NID:9153840; PIDN:AAA2701

A;Note: sequence extracted from NCBI backbone (NCBI:75635, NCBI:75636)

R;Talkington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.E.

Infect. Immun. 59, 1285-1289, 1991

A;Title: A 43-kilodalton pneumococcal surface protein, PspA: isolation, protective ability

A;Reference number: A60282; MUID:91169598; PMID:2004810

A;Accession: A60282

A;Molecule type: protein

A;Residues: 32-76 <TAL>

A;Experimental source: strain JY2008

C;Genetics:

A;Gene: pspA

F;1-31/Domain: signal sequence #status predicted <SIG>

F;32-619/Product: surface protein pspA #status predicted <MAT>

F;411-430/Domain: cpl repeat homology <CP01>

F;431-450/Domain: cpl repeat homology <CP02>

F;451-470/Domain: cpl repeat homology <CP03>

F;471-490/Domain: cpl repeat homology <CP04>

F;491-510/Domain: cpl repeat homology <CP05>

F;511-530/Domain: cpl repeat homology <CP06>

F;531-550/Domain: cpl repeat homology <CP07>

F;551-570/Domain: cpl repeat homology <CP08>

F;571-591/Domain: cpl repeat homology <CP09>

F;592-611/Domain: cpl repeat homology <CP10>

Query Match

Best Local Similarity 36.7%; Score 197; DB 2; Length 619;

Matches 50; Conservative 18; Mismatches 25; Indels 18; Gaps 3;

Qy 6 AGLENLLSTLDPEGKTQDELKQ-----AAAEALNKKVEALPNQVAELE 49
Db 210 AELENQVHRLEQELKEIDSESEYAKSGFRAPLQSKLDAAKKALS-KLEELSDKIDELD 268

Qy 50 BELSKLENLQDA-ETNHVEDYIKGLEBEATATQAELEKTPKELDAAINE 99

Db 269 AEIAKLEQLKAAEENNVEDYFKEGLEKTTAAKKAEELEKTEADLUKAVNE 319

RESULT 4

D71453

hypothetical protein PH0283 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: D71453

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: D71453

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-279 <KAW>

A;Cross-references: UNIPROT:O58021; GB:AP000001; NID:93236128; PIDN:BA29355.1; PID:g325

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH0283

Query Match

Best Local Similarity 20.9%; Score 112; DB 2; Length 279;

Matches 38; Conservative 21; Mismatches 42; Indels 18; Gaps 4;

Qy 1 LEKAGAGLENLLSTLDPEGKTQDELKQAAAEALN-----KKVEALPNQVAELEEL 52
Db 164 LEKAKEIEELKERIETLEKEKKELEKESVKLMEYAKAKKVBELKKEYEKS 223

Qy 53 SKLEDNLKDAETNHVE-DYIKGLEEAEIATQAELE-----KTPKELDAALNELGPDG 104

Db 224 REIEGRKDYEEKIRELEEBEKKGLEEKINLENRIENLKNIGIRSAKE---ALERLLEEG 279

RESULT 5

T14156

kinesin-related protein - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14156

R;Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.

Cell 91, 357-366, 1997

A;Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromoso

A;Reference number: Z17893; MUID:98028574; PMID:9363944

A;Accession: T14156

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2954 <WOO>

A;Cross-references: UNIPROT:O42263; EMBL:AF027728; NID:g2586070; PID:g2586071; PIDN:AAC6

C;Genetics:

A;Gene: XCENP-E

C;Superfamily: centromere protein E; kinesin motor domain homology

Query Match

Best Local Similarity 20.8%; Score 111.5; DB 2; Length 2954;

Matches 33; Conservative 21; Mismatches 39; Indels 21; Gaps 3;

Qy 2 EKAGAGLENLLSTLDPE-----GKTQDELKQAAAEALNKKVEALPNQVAELEELSKLED 57
Db 1952 EQALANTEHLRETLLKSKDLALGKMEQERDEAA-----NKVIALTKMSLEEQINENVT 2005

Query Match

Best Local Similarity 45.0%; Pred. No. 1.6e-05;

Matches 50; Conservative 18; Mismatches 25; Indels 18; Gaps 3;

Qy 6 AGLENLLSTLDPEGKTQDELKQ-----AAAEALNKKVEALPNQVAELE 49
Db 210 AELENQVHRLEQELKEIDSESEYAKSGFRAPLQSKLDAAKKALS-KLEELSDKIDELD 268

Qy 50 BELSKLENLQDA-ETNHVEDYIKGLEBEATATQAELEKTPKELDAAINE 99

Db 269 AEIAKLEQLKAAEENNVEDYFKEGLEKTTAAKKAEELEKTEADLUKAVNE 319

RESULT 4

D71453

hypothetical protein PH0283 - Pyrococcus horikoshii

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 20:04:33 ; Search time 14.1144 Seconds
(without alignments)
736.230 Million cell updates/sec

Title: US-10-674-755-24
Perfect score: 537
Sequence: 1 LEKAGAGLELLSTLDPEGK.....TPKELDAALNELGPDGDEEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 306 | 57.0 | 744 | 2 F95013 | pneumococcal surfa |
| 2 | 197 | 36.7 | 619 | 2 A97887 | surface protein ps |
| 3 | 197 | 36.7 | 619 | 2 A41971 | surface protein ps |
| 4 | 112 | 20.9 | 279 | 2 D71453 | hypothetical prote |
| 5 | 111.5 | 20.8 | 2954 | 2 T14156 | kinesin-related pr |
| 6 | 110.5 | 20.6 | 1961 | 1 A61231 | myosin heavy chain |
| 7 | 110 | 20.5 | 1938 | 1 A40997 | myosin heavy chain |
| 8 | 109 | 20.3 | 388 | 2 A46173 | Mrp4 protein - Str |
| 9 | 108.5 | 20.2 | 1964 | 2 A52822 | nonmuscle myosin I |
| 10 | 108 | 20.1 | 407 | 2 S23325 | M2 protein precurs |
| 11 | 107 | 19.9 | 1006 | 2 C70445 | Arpase subunit of |
| 12 | 107 | 19.9 | 1931 | 2 A59234 | slow myosin heavy |
| 13 | 105 | 19.6 | 1992 | 2 A47297 | myosin heavy chain |
| 14 | 105 | 19.6 | 2139 | 2 T18296 | myosin heavy chain |
| 15 | 104 | 19.4 | 415 | 2 S35760 | fcra protein precu |
| 16 | 104 | 19.4 | 1959 | 1 A33977 | myosin heavy chain |
| 17 | 104 | 19.4 | 1976 | 2 A59252 | myosin heavy chain |
| 18 | 103.5 | 19.3 | 281 | 2 F75216 | hypothetical prote |
| 19 | 103.5 | 19.3 | 779 | 2 C96805 | hypothetical prote |
| 20 | 103.5 | 19.3 | 1938 | 2 J05421 | smooth muscle myos |
| 21 | 103.5 | 19.3 | 1972 | 2 J05420 | smooth muscle myos |
| 22 | 103.5 | 19.3 | 1979 | 1 S03166 | myosin heavy chain |
| 23 | 103.5 | 19.3 | 2007 | 1 B43402 | myosin heavy chain |
| 24 | 103 | 19.2 | 501 | 2 A38650 | myosin heavy chain |
| 25 | 102 | 19.0 | 399 | 2 E71169 | hypothetical prote |
| 26 | 102 | 19.0 | 405 | 2 A33939 | Pc gamma (IgG) rec |
| 27 | 101.5 | 18.9 | 1177 | 2 B75150 | chromosome segrega |
| 28 | 101 | 18.8 | 516 | 2 B84709 | hypothetical prote |
| 29 | 100.5 | 18.7 | 1940 | 2 A59287 | myosin heavy chain |

ALIGNMENTS

RESULT 1

F95013
pneumococcal surface protein A [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95013
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95013
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <KUR>
A:Cross-references: UNIPROT:Q97T39; GB:AE005672; PIDN:AAK74303.1; PID:g14971584; GSPDB:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0117

| | | | | |
|-----------------------|-------|--|--------|----------------|
| Query Match | 57.0% | Score 306; | DB 2; | Length 744; |
| Best Local Similarity | 63.9% | Pred No. 2.3e-12; | | |
| Matches | 69; | Conservative | 12; | Mismatches 23; |
| | | | Indels | 4; |
| | | | Gaps | 2; |
| QY | 1 | LEKAGAGLELLSTLDPEGKTQDELKFAAEALNKKVKEALPNQVAEELEELSLESLKLEDLNK | 60 | |
| DB | 346 | LAKQTELEKLLDSLDPEGKTQDELKFAAEALNKKVKEALPNQVAEELEELSLESLKLEDLNK | 405 | |
| QY | 61 | DAETHVEDYIKESGLEAIAATKQAELEKTPKELDAALNELGPDGDEEE | 108 | |
| DB | 406 | GADS---ED-DTAALQNKLATKAALEKTKQELDAALNELGPDGDEEE | 449 | |

RESULT 2

A97887
surface protein pspA precursor [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A97887
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
J. P.; Sun, P.M.; Winkler, M.E.
Y. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A97887
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-619 <KUR>

```

DT 28-OCT-1997 (first entry)
XX Streptococcus pneumoniae PspA central region.
DE
XX
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
XX Streptococcus pneumoniae; strain Bg7561.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 44
FT /note= "unidentified amino acid"
XX
XX WO9709994-A1.
XX
XX 20-MAR-1997.
XX
XX 16-SEP-1996; 96WO-US014819.
XX
XX 15-SEP-1995; 95US-00529055.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
XX
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
XX Example 6; Fig 13; 296pp; English.
XX
XX This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7561.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 184 AA;
XX
XX Query Match 77.4%; Score 415.5; DB 2; Length 184;
XX Best Local Similarity 82.2%; Pred. No. 1.8e-28;
XX Matches 88; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
XX
QY 2 EKAGAGLENLLSTLDPEGKTODELDKAAAEALNKKVEALPNQVAEELEELSKLEDNLKD 61
XX :|
DB 1 KKQKVNLENLLST-DPGKQTODELDKGAEEALNKKVEALPNVXELEELSPPEDNLKD 59
XX
QY 62 AETHNVEDYIKEGLEEAATKQAELEKTPKSLDAALNELGPDGDEEE 108
XX
DB 60 AETHNVEDYIKFLEEAATKQAELEETPQEVDAALNDLVPDGGEEE 106
XX
Search completed: November 17, 2005, 20:19:42
Job time : 77.7468 secs

```


CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is EF5688 pneumococcal
 CC surface protein A (PspA) used in the exemplification of the invention
 XX
 SQ Sequence 458 AA;

Query Match 87.0%; Score 467; DB 7; Length 458;
 Best Local Similarity 88.9%; Pred. No. 1.6e-32;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 60
 DB 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 335
 QY 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 108
 DB 336 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 383

RESULT 11
 ADK52495
 ID ADK52495 standard; protein; 653 AA.

XX ADK52495;

XX 20-MAY-2004 (first entry)

XX PspA molecule from the Rx1 strain of Streptococcus pneumoniae.

XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
 KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
 KW Hodgkin's disease.

XX Streptococcus pneumoniae.

XX WO2004016231-A2.

XX 26-FEB-2004.

XX 17-FEB-2003; 2003WO-US008199.

XX 15-MAR-2002; 2002US-0365351P.

XX (UABR-) UAB RES FOUND.

XX Briles DE;

XX WPI; 2004-192068/18.

XX Treating Streptococcus pneumoniae infection in a subject lacking a
 functional spleen comprises administering an antibody that recognizes
 PT pneumococcal surface protein A (PspA) or its binding portion.

XX Claim 17; SEQ ID NO 1; 41pp; English.

XX The present invention relates to treating Streptococcus pneumoniae
 CC infection in a subject lacking a functional spleen comprises
 CC administering an antibody that recognizes pneumococcal surface protein A
 CC (PspA) or its binding portion. The method is useful for treating or
 CC preventing Streptococcus pneumoniae infection in a subject lacking a
 CC functional spleen. The disease-associated injury is especially due to
 CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
 CC anemia or Hodgkin's disease. The present sequence represents PspA
 CC molecule from the Rx1 strain of Streptococcus pneumoniae.

XX Sequence 653 AA;

Query Match 87.0%; Score 467; DB 8; Length 653;
 Best Local Similarity 88.9%; Pred. No. 2.4e-32;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 60
 DB 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 335
 QY 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 108

DB 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 335
 QY 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 108
 DB 336 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 383

RESULT 12

ADOS2080

ID ADO52080 standard; protein; 653 AA.

XX ADO52080;

XX 12-AUG-2004 (first entry)

XX S. pneumoniae strain EF5688 PspA protein.

XX Immunogenic composition; vaccine; Th2-type immune response;
 KW pneumococcal surface protein A; PspA.

XX Streptococcus pneumoniae.

XX Key Location/Qualifiers

XX Peptide 1..31

XX Protein /label= Signal_peptide

XX Domain 32..653

XX /note= "S. pneumoniae strain EF5688 mature PspA protein"

XX 110..384

XX /note = PspA alpha-helical domain

XX US20040101531-A1.

XX 27-MAY-2004.

XX 15-APR-2003; 2003US-00414532.

XX 16-APR-2002; 2002US-0372710P.

XX (CURT/) CURTISS R.

XX (KANG/) KANG H Y.

XX Curtiss R, Kang HY;

XX WPI; 2004-399655/37.

XX N-PSDB; ADO52067.

XX New vaccine comprising a live attenuated strain of pathogenic gram-
 negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 or bacteria.

XX Example 5; SEQ ID NO 26; 94pp; English.

XX The invention relates to immunogenic compositions and vaccines comprising
 CC a live attenuated strain of pathogenic gram negative bacteria that
 CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
 CC response in a vertebrate against pathogens, e.g., helminths, fungi,
 CC viruses, protozoans or bacteria. The present sequence is Streptococcus
 CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA). This
 CC sequence is used in the exemplification of the invention.

XX Sequence 653 AA;

Query Match 87.0%; Score 467; DB 8; Length 653;

Best Local Similarity 88.9%; Pred. No. 2.4e-32;

Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LEKAGAGLENLSTLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 60
 DB 276 LEDAELEKVLATLDPEGKTQDELDEKAAAEALNKKVEALPNQVALEELSKLEDNLK 335
 QY 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNKLPGDGDDEE 108

DR WPI; 2004-192068/18.
XX Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX Claim 17; SEQ ID NO 2; 41pp; English.
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rxi strain of Streptococcus
XX pneumoniae.
XX Sequence 369 AA;
SQ
Query Match 87.0%; Score 467; DB 8; Length 369;
Best Local Similarity 88.9%; Pred. No. 1.2e-32;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LEKAGAGLENLSTLDPEGKTQDELDKAAAEALNKVEALPNQVAELEEEELSKLEDNLK 60
DB 245 LEDAELEKVLATLDPEGKTQDELDKAAAEALNKVEALQNVAELEEEELSKLEDNLK 304
QY 61 DAETHNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
DB 305 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 352
RESULT 9
AAW14592
ID AAW14592 standard; protein; 458 AA.
XX AC AAW14592;
XX DT 17-OCT-2003 (revised)
XX DT 27-OCT-1997 (first entry)
XX DE Streptococcus pneumoniae PspA surface protein.
XX KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
XX KW bacteraemia; pneumonia.
XX OS Streptococcus pneumoniae; strain Ef5668.
XX PN WO9709994-A1.
XX PD 20-MAR-1997.
XX PF 16-SEP-1996; 96WO-US014819.
XX PR 15-SEP-1995; 95US-00529055.
XX PA (UABR-) UAB RES FOUND.
XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
XX PI Hollingshead S, Tart R, Brooks-Walter A;
XX DR WPI; 1997-202002/18.
XX DR N-PSDB; AAT61724.
XX ST Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX PS Disclosure; Fig 13; 296pp; English.
XX This sequence comprises the pneumococcal surface protein A (pspA) of
CC Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the

CC pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be
CC used in vaccines to protect animals against S. pneumoniae infection and
CC hence for the prevention of diseases such as otitis media, meningitis,
CC bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX SQ Sequence 458 AA;
Query Match 87.0%; Score 467; DB 2; Length 458;
Best Local Similarity 88.9%; Pred. No. 1.6e-32;
Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LEKAGAGLENLSTLDPEGKTQDELDKAAAEALNKVEALPNQVAELEEEELSKLEDNLK 60
DB 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNKVEALQNVAELEEEELSKLEDNLK 335
QY 61 DAETHNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
DB 336 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 383
RESULT 10
ABW02626
ID ABW02626 standard; protein; 458 AA.
XX AC ABW02626;
XX DT 12-FEB-2004 (first entry)
XX DE Ef5668 pneumococcal surface protein A (PspA).
XX KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
XX KW immunological; gene therapy; immunostimulant.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Misc-difference 458 /note= "Encoded by GC"
FT FT
XX US\$592876-B1.
XX PD 15-JUL-2003.
XX PF 15-SEP-1995; 95US-00529055.
XX PR 20-APR-1993; 93US-00048896.
XX PR 06-JUN-1995; 95US-00465746.
XX PA (UABR-) UAB RES FOUND.
XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX DR WPI; 2003-862841/80.
XX DR N-PSDB; AAD64535.
XX PT Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX Example 6; SEQ ID NO 73; 121pp; English.
XX The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response

XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
 KW immunological; gene therapy; immunostimulant.

OS Unidentified.

XX US5592876-B1.

XX PD 15-JUL-2003.

XX PF 15-SEP-1995; 95US-00529055.

XX PR 20-APR-1993; 93US-00048896.

XX PR 06-JUN-1995; 95US-00465746.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX DR WPI; 2003-862841/80.

XX Immunological composition for obtaining expression products used for
 PT detecting the presence of Streptococcus pneumoniae or its strain,
 PT comprises at least two different full length isolated gene encoding
 PT pneumococcal surface protein A.

XX Example 6; SEQ ID NO 70; 121bp; English.

XX The present invention relates to an immunological composition comprising
 CC at least 2 different full length isolated genes encoding pneumococcal
 CC surface protein A (PspAs) from different groups based on restriction
 CC fragment polymorphism analysis. The invention is useful for obtaining
 CC expression products by recombinant techniques to detect, determine,
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its
 CC strain. The expression product is useful for preparing antigenic,
 CC immunological or vaccine compositions, for eliciting antibodies, an
 CC immunological response (other than or additional to antibodies) or a
 CC protective response (including antibody or other immunological response
 CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is Ef5668c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention

XX SQ Sequence 232 AA;

Query Match 87.0%; Score 467; DB 7; Length 232;
 Best Local Similarity 88.9%; Pred. No. 7.2e-33;
 Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNOVALEBEELSLEDNLK 60

Db 51 LEDAELELEKVLATLDPEGKTQDELKKEAAEALNKKVEALPNOVALEBEELSLEDNLK 110

Qy 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108

Db 111 DASTNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 158

RESULT 7

AD052055

ID AD052055 standard; protein; 275 AA.

XX AC AD052055;

XX DT 12-AUG-2004 (first entry)

XX DE S. pneumoniae strain EF5688 PspA alpha helical domain.

XX KW Immunogenic composition; vaccine; Th2-type immune response ;

XX KW pneumococcal surface protein A; PspA.

XX OS Streptococcus pneumoniae.

XX

PN US2004101531-A1.

XX PD 27-MAY-2004.

XX PF 15-APR-2003; 2003US-00414532.

XX PR 16-APR-2002; 2002US-0372710P.

XX PA (CURT/) CURTISS R.

XX PA (KANG/) KANG H Y.

XX PI Curtiss R, Kang HY;

XX DR WPI; 2004-399655/37.

XX New vaccine comprising a live attenuated strain of pathogenic gram-
 PT negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 PT or bacteria.

XX PS Claim 17; SEQ ID NO 1; 94pp; English.

XX The invention relates to immunogenic compositions and vaccines comprising
 CC a live attenuated strain of pathogenic gram negative bacteria that
 CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
 CC response in a vertebrate against pathogens, e.g., helminths, fungi,
 CC viruses, protozoans or bacteria. The present sequence is Streptococcus
 CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
 CC helical domain. This sequence is used in the invention.

XX SQ Sequence 275 AA;

Query Match 87.0%; Score 467; DB 8; Length 275;

Best Local Similarity 88.9%; Pred. No. 8.8e-33;

Matches 96; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LEKAGAGLENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNOVALEBEELSLEDNLK 60

Db 167 LEDAELELEKVLATLDPEGKTQDELKKEAAEALNKKVEALPNOVALEBEELSLEDNLK 226

Qy 61 DAETNHVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108

Db 227 DASTNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 274

RESULT 8

ADK52496

ID ADK52496 standard; protein; 369 AA.

XX AC ADK52496;

XX DT 20-MAY-2004 (first entry)

XX DE alpha helical region PspA molecule from the Rx1 strain.

XX KW Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;

XX KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;

XX KW Hodgkin's disease.

XX OS Streptococcus pneumoniae.

XX PN WO2004016231-A2.

XX PD 26-FEB-2004.

XX PF 17-FEB-2003; 2003WO-US008199.

XX PR 15-MAR-2002; 2002US-0365351P.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE;

XX

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
|||||
Db 8255 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 8302

RESULT 4
ABW02621
ID ABW02621 standard; protein; 211 AA.

AC ABW02621;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bg11703c pneumococcal surface protein A (PspA) central region.
DE
KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX
OS Unidentified.
XX
PN US6592876-B1.
XX
PD 15-JUL-2003.

PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.

XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.

PS Example 6; SEQ ID NO 67; 121pp; English.
XX
CC The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg11703c
CC pneumococcal surface protein A (PspA) central region. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 211 AA;

Query Match 95.2%; Score 511; DB 7; Length 211;
Best Local Similarity 96.3%; Pred. No. 9.1e-37;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEKAGALENLLSTLDPEGKTQDELKDAEAELNKKVEALPNOVAEEELSKLEDNLK 60
|||||
Db 25 LEKAEAELENLLSTLDPEGKTQDELKDAEAELNKKVEALPNOVSEEEELSKLEDNLK 84

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
|||||
Db 85 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 132

RESULT 5

AAW14587
ID AAW14587 standard; protein; 238 AA.
XX
AC AAW14587;
XX
DT 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Bg11703.
XX
PN WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
PA (UABR-) UAB RES FOUND.

PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
XX
PT Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
PS Example 6; Fig 13; 296pp; English.
XX
CC This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg11703.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 238 AA;
SQ
Query Match 95.2%; Score 511; DB 2; Length 238;
Best Local Similarity 96.3%; Pred. No. 1.1e-36;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEKAGALENLLSTLDPEGKTQDELKDAEAELNKKVEALPNOVAEEELSKLEDNLK 60
|||||
Db 25 LEKAEAELENLLSTLDPEGKTQDELKDAEAELNKKVEALPNOVSEEEELSKLEDNLK 84

QY 61 DAETNHVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108
|||||
Db 85 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 132

RESULT 6
ABW02624
ID ABW02624 standard; protein; 232 AA.

XX
AC ABW02624;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ef5668c pneumococcal surface protein A (PspA) central region.

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 76.7468 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-24

Perfect score: 537

Sequence: 1 LEKAGAGLENLLTLDPEK.....TPKELDAALNELGPDGDEE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|------------------------|
| 1 | 530 | 98.7 | 212 | 2 AAW14588 | Aaw14588 Streptococcus |
| 2 | 530 | 98.7 | 212 | 7 ABW02622 | Abw02622 Bg7817c p |
| 3 | 530 | 98.7 | 8991 | 6 ABU08487 | Abu08487 S. pneumo |
| 4 | 511 | 95.2 | 211 | 7 ABW02621 | Abw02621 Bg11703c |
| 5 | 511 | 95.2 | 238 | 2 AAW14587 | Aaw14587 Streptococcus |
| 6 | 467 | 87.0 | 232 | 7 ABW02624 | Abw02624 Ef5668c p |
| 7 | 467 | 87.0 | 275 | 8 ADO52055 | Ado52055 S. pneumo |
| 8 | 467 | 87.0 | 369 | 8 ADK52496 | Adk52496 alpha hel |
| 9 | 467 | 87.0 | 458 | 2 AAW14592 | Aaw14592 Streptococcus |
| 10 | 467 | 87.0 | 458 | 7 ABW02626 | Abw02626 Ef5668 pn |
| 11 | 467 | 87.0 | 653 | 8 ADK52495 | Adk52495 PspA mole |
| 12 | 467 | 87.0 | 653 | 8 ADO52080 | Ado52080 S. pneumo |
| 13 | 456.5 | 85.0 | 233 | 2 AAW14590 | Aaw14590 Streptococcus |
| 14 | 439 | 81.8 | 185 | 7 ABW02623 | Abw02623 Bg7561c p |
| 15 | 415.5 | 77.4 | 184 | 2 AAW14589 | Aaw14589 Streptococcus |
| 16 | 317 | 59.0 | 213 | 7 ABW02601 | Abw02601 Bg8090c p |
| 17 | 306.5 | 57.1 | 459 | 8 ADO15316 | Ado15316 S. pneumon |
| 18 | 306 | 57.0 | 213 | 2 AAW14567 | Aaw14567 Streptococcus |
| 19 | 306 | 57.0 | 416 | 8 ADK52498 | Adk52498 alpha hel |
| 20 | 306 | 57.0 | 526 | 8 ADK52497 | Adk52497 PspA mole |
| 21 | 306 | 57.0 | 744 | 6 ABU00449 | Abu00449 S. pneumo |
| 22 | 306 | 57.0 | 744 | 8 ADM92054 | Adm92054 S. pneumon |
| 23 | 306 | 57.0 | 745 | 3 AAY81652 | Aay81652 Streptococcus |
| 24 | 305 | 56.8 | 641 | 2 AAW61217 | Aaw61217 Streptococcus |
| 25 | 305 | 56.8 | 641 | 5 ABP54636 | Abp54636 S. pneumo |

| | | | | | |
|----|-------|------|-----|------------|------------------------|
| 26 | 305 | 56.8 | 641 | 7 ADC45241 | Adc45241 S. pneumo |
| 27 | 300 | 55.9 | 197 | 7 ABW02598 | Abw02598 Ac122c pn |
| 28 | 295 | 54.9 | 233 | 7 ABW02606 | Abw02606 Ef1019c p |
| 29 | 288 | 53.6 | 233 | 2 AAW14572 | Aaw14572 Streptococcus |
| 30 | 287.5 | 53.5 | 119 | 2 AAW46291 | Aaw46291 Pneumococcus |
| 31 | 287.5 | 53.5 | 215 | 2 AAW14563 | Aaw14563 Streptococcus |
| 32 | 287.5 | 53.5 | 215 | 7 ABW02597 | Abw02597 Atcc6303c |
| 33 | 282.5 | 52.6 | 196 | 2 AAW14564 | Aaw14564 Streptococcus |
| 34 | 272 | 50.7 | 487 | 8 ADR04321 | Adr04321 Streptococcus |
| 35 | 272 | 50.7 | 489 | 8 ADO52088 | Ado52088 Streptococcus |
| 36 | 272 | 50.7 | 524 | 8 ADO52082 | Ado52082 E. coli B |
| 37 | 272 | 50.7 | 627 | 8 ADO52129 | Ado52129 E. coli B |
| 38 | 262.5 | 48.9 | 290 | 8 ADO52119 | Ado52119 pYA3637 b |
| 39 | 262.5 | 48.9 | 298 | 8 ADO52127 | Ado52127 pYA3637 b |
| 40 | 261 | 48.6 | 230 | 8 ADO52086 | Ado52086 S. pneumo |
| 41 | 261 | 48.6 | 230 | 8 ADR04319 | Adr04319 Streptococcus |
| 42 | 197 | 36.7 | 315 | 2 AAY04375 | Aay04375 Streptococcus |
| 43 | 197 | 36.7 | 619 | 2 AAR63437 | Aar63437 Pneumococcus |
| 44 | 197 | 36.7 | 619 | 2 AAR87598 | Aar87598 Pneumococcus |
| 45 | 197 | 36.7 | 619 | 2 AAR86911 | Aar86911 Pneumococcus |

ALIGNMENTS

RESULT 1
AAW14588
ID AAW14588 standard; protein; 212 AA.
XX
AC AAW14588;
XX
DT 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)
XX
DE Streptococcus pneumoniae PspA central region.
XX
KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Bg7817.
XX
PN WO9709994-A1.
XX PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
(UABR-) UAB RES FOUND.
Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
Hollingshead S, Tart R, Brooks-Walter A;
WPI; 1997-202002/18.

Streptococcus pneumoniae surface protein PspC and truncated PspA - used in vaccines for protecting animals against S.pneumoniae infection.
Example 6; Fig 13; 296pp; English.

This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Bg7817. Comparison of the N-terminal and central regions (AAW14533-57 and AAW14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine

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; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: UNSURE
; FEATURE:
; LOCATION: (2)
; OTHER INFORMATION: Xaa at position 2 is unknown
US-10-299-636-62

Query Match          61.0%; Score 325; DB 15; Length 213;
Best Local Similarity 65.7%; Pred. No. 1.9e-16;
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELESELSKLEDLNKK 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 LAKKQTELEKLDLNDPEGKTQDELDKAAAEALDKADELPNKVADLEKISNLEILG 118
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEEE 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 GADP---ED-DTAALPNKLTATKAEFEKTPKELDAALNELGPDGDEEE 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-702-305A-18
; Sequence 18, Application US/10702305A
; Publication No. US20040213803A1
; GENERAL INFORMATION:
; APPLICANT: Michael C. Chen
; APPLICANT: Chuang-Jiun Chiou
; APPLICANT: Zhongming Li
; APPLICANT: Dong-Sheng Chen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR
; TITLE OF INVENTION: PREVENTING PNEUMOCOCCAL INFECTION
; FILE REFERENCE: 12844-002001
; CURRENT APPLICATION NUMBER: US/10/702,305A
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/424,497
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence
US-10-702-305A-18

Query Match          60.5%; Score 322.5; DB 16; Length 459;
Best Local Similarity 59.1%; Pred. No. 6.8e-16;
Matches 68; Conservative 16; Mismatches 20; Indels 11; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELDKAAE-----AELNKKVEALPNQVSELESELSKLE 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 LEDAELELEKVLATLDPEGKTQDELDKAAEADANIEALQNKVADLENKVAELDKVTRLQ 404
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 57 DNLKDAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDG 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 SLDKDAENNVEDYVKEGLDKALTDKKVELNNTQKALDTAOKALDTALNELGPDG 459
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-674-755-21
; Sequence 21, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
```

```
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-21

Query Match          60.2%; Score 321; DB 15; Length 104;
Best Local Similarity 65.7%; Pred. No. 1.7e-16;
Matches 71; Conservative 11; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELESELSKLEDLNKK 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 LAKKQTELEKLDLNDPEGKTQDELDKAAAEALDKADELPNKVADLEKISNLEILG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEEE 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GADP---ED-DTAALPNKLTATKAELEKTPKELDAALNELGPDGDEEE 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: November 17, 2005, 20:29:18
Job time : 72.832 secs
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Oy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSLEDNLK 60
Db 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNKKVEALQNVAELEELSLEDNLK 335
Oy 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
Db 336 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 383

RESULT 10
US-10-414-532-26
; Sequence 26, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-26

Query Match 90.6%; Score 483; DB 16; Length 653;
Best Local Similarity 90.7%; Pred. No. 1.5e-27;
Matches 98; Conservative 5; Mismatches 27; Indels 0; Gaps 0;

Oy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSLEDNLK 60
Db 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNKKVEALQNVAELEELSLEDNLK 335
Oy 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
Db 336 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 383

RESULT 11
US-10-674-755-26
; Sequence 26, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)-(108)
; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
US-10-674-755-26

Query Match 86.5%; Score 461; DB 15; Length 108;
Best Local Similarity 88.0%; Pred. No. 8.2e-27;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSLEDNLK 60
```

```
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNVXSELEELSPPEDNLK 60
Oy 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
Db 61 DAETNNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 108

RESULT 12
US-10-299-636-84
; Sequence 84, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (45)
; OTHER INFORMATION: Xaa at position 45 is unknown
US-10-299-636-84

Query Match 81.6%; Score 435; DB 15; Length 185;
Best Local Similarity 83.2%; Pred. No. 1.2e-24;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Oy 2 EKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSLEDNLK 61
Db 1 KQKVNLENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNVXSELEELSPPEDNLK 60
Oy 62 AETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
Db 61 AETNNVEDYIKGLEEAIATKQAELEETPQEVDAALNDLVPDGGEE 107

RESULT 13
US-10-299-636-62
; Sequence 62, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
```

Db 60 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106

RESULT 6

US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:

; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-25

Query Match 90.6%; Score 483; DB 15; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.9e-28;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKVKVEALPNQVSELEELSLEDNLK 60

Db 1 LEDAELELEKVLATLDPEGKTQDELDKAAAEALNKVKVEALQNVAELEELSLEDNLK 60

QY 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 7

US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:

; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-85

Query Match 90.6%; Score 483; DB 15; Length 232;
Best Local Similarity 90.7%; Pred. No. 4.6e-28;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKVKVEALPNQVSELEELSLEDNLK 60

Db 51 LEDAELELEKVLATLDPEGKTQDELDKAAAEALNKVKVEALQNVAELEELSLEDNLK 110

QY 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108
Db 111 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 158

RESULT 8

US-10-414-532-1
; Sequence 1, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:

; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-1

Query Match 90.6%; Score 483; DB 16; Length 275;
Best Local Similarity 90.7%; Pred. No. 5.5e-28;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKVKVEALPNQVSELEELSLEDNLK 60

Db 167 LEDAELELEKVLATLDPEGKTQDELDKAAAEALNKVKVEALQNVAELEELSLEDNLK 226

QY 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

Db 227 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 274

RESULT 9

US-10-299-636-88
; Sequence 88, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:

; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-88

Query Match 90.6%; Score 483; DB 15; Length 458;
Best Local Similarity 90.7%; Pred. No. 9.8e-28;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```
US-10-299-636-82
; Sequence 82, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-82

Query Match 100.0%; Score 533; DB 15; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.4e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEKAAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSLEDNLK 60
Db 25 LEKAAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSLEDNLK 84
Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db 85 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 132

RESULT 3
US-10-674-755-24
; Sequence 24, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-24

Query Match 95.9%; Score 511; DB 15; Length 108;
Best Local Similarity 96.3%; Pred. No. 1.7e-30;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LEKAAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSLEDNLK 60
Db 1 LEKAGAGLNLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVAEELSLEDNLK 60
Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108

US-10-299-636-83
; Sequence 83, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-83

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Best Local Similarity 95.4%; Pred. No. 1.2e-29;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 28 LEKAGAGLNLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVAEELSLEDNLK 87
Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db 88 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 135

RESULT 4
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; Sequence 22, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-22

Query Match 94.2%; Score 502; DB 15; Length 106;
Best Local Similarity 98.1%; Pred. No. 7.5e-30;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Db 1 LEKAAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSLEDNLK 59
Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 71.832 Seconds
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629.082 Million cell updates/sec

Title: US-10-674-755-23
Perfect score: 533
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 533 | 100.0 | 211 | 15 | US-10-299-636-82 |
| 3 | 511 | 95.9 | 108 | 15 | US-10-674-755-24 |
| 4 | 504 | 94.6 | 212 | 15 | US-10-299-636-83 |
| 5 | 502 | 94.2 | 106 | 15 | US-10-674-755-22 |
| 6 | 483 | 90.6 | 108 | 15 | US-10-674-755-25 |
| 7 | 483 | 90.6 | 232 | 15 | US-10-299-636-85 |
| 8 | 483 | 90.6 | 275 | 15 | US-10-414-532-1 |
| 9 | 483 | 90.6 | 458 | 15 | US-10-299-636-88 |
| 10 | 483 | 90.6 | 653 | 16 | US-10-414-532-26 |
| 11 | 461 | 86.5 | 108 | 15 | US-10-674-755-26 |
| Sequence 23, Appl | | | | | |
| Sequence 82, Appl | | | | | |
| Sequence 24, Appl | | | | | |
| Sequence 83, Appl | | | | | |
| Sequence 22, Appl | | | | | |
| Sequence 25, Appl | | | | | |
| Sequence 85, Appl | | | | | |
| Sequence 1, Appl | | | | | |
| Sequence 88, Appl | | | | | |
| Sequence 26, Appl | | | | | |

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| 12 | 435 | 81.6 | 185 | 15 | US-10-299-636-84 | Sequence 84, Appl |
| 13 | 325 | 61.0 | 213 | 15 | US-10-299-636-62 | Sequence 62, Appl |
| 14 | 322.5 | 60.5 | 459 | 16 | US-10-702-305A-18 | Sequence 18, Appl |
| 15 | 321 | 60.2 | 104 | 15 | US-10-674-755-21 | Sequence 21, Appl |
| 16 | 319 | 59.8 | 104 | 15 | US-10-674-755-20 | Sequence 20, Appl |
| 17 | 314 | 58.9 | 744 | 10 | US-09-769-787-184 | Sequence 184, Appl |
| 18 | 314 | 58.9 | 744 | 17 | US-10-472-928-32 | Sequence 32, Appl |
| 19 | 313 | 58.7 | 197 | 15 | US-10-299-636-59 | Sequence 59, Appl |
| 20 | 313 | 58.7 | 641 | 9 | US-09-765-272-160 | Sequence 160, Appl |
| 21 | 313 | 58.7 | 641 | 20 | US-11-106-649-160 | Sequence 160, Appl |
| 22 | 298 | 55.9 | 102 | 15 | US-10-674-755-18 | Sequence 18, Appl |
| 23 | 285 | 53.5 | 233 | 15 | US-10-299-636-67 | Sequence 67, Appl |
| 24 | 283 | 53.1 | 487 | 16 | US-10-414-532-34 | Sequence 34, Appl |
| 25 | 283 | 53.1 | 487 | 16 | US-10-414-533-21 | Sequence 21, Appl |
| 26 | 283 | 53.1 | 524 | 16 | US-10-414-532-28 | Sequence 28, Appl |
| 27 | 279.5 | 52.4 | 119 | 15 | US-10-674-755-27 | Sequence 27, Appl |
| 28 | 279.5 | 52.4 | 215 | 15 | US-10-299-636-58 | Sequence 58, Appl |
| 29 | 273.5 | 51.3 | 290 | 16 | US-10-414-532-65 | Sequence 65, Appl |
| 30 | 272 | 51.0 | 230 | 16 | US-10-414-532-32 | Sequence 32, Appl |
| 31 | 272 | 51.0 | 230 | 16 | US-10-414-533-19 | Sequence 19, Appl |
| 32 | 238 | 44.7 | 80 | 15 | US-10-674-755-19 | Sequence 19, Appl |
| 33 | 211 | 39.6 | 354 | 15 | US-10-299-636-105 | Sequence 105, Appl |
| 34 | 211 | 39.6 | 588 | 15 | US-10-299-636-96 | Sequence 96, Appl |
| 35 | 211 | 39.6 | 619 | 10 | US-09-882-774-1 | Sequence 1, Appl |
| 36 | 211 | 39.6 | 619 | 15 | US-10-282-122A-73702 | Sequence 73702, A |
| 37 | 211 | 39.6 | 619 | 16 | US-10-414-532-72 | Sequence 72, Appl |
| 38 | 199 | 37.3 | 204 | 15 | US-10-299-636-66 | Sequence 66, Appl |
| 39 | 195 | 36.6 | 99 | 15 | US-10-674-755-11 | Sequence 11, Appl |
| 40 | 191.5 | 35.9 | 100 | 15 | US-10-674-755-12 | Sequence 12, Appl |
| 41 | 190 | 35.6 | 198 | 15 | US-10-299-636-76 | Sequence 76, Appl |
| 42 | 184 | 34.5 | 141 | 14 | US-10-254-995-2 | Sequence 2, Appl |
| 43 | 184 | 34.5 | 589 | 9 | US-09-748-875-14 | Sequence 14, Appl |
| 44 | 184 | 34.5 | 589 | 10 | US-09-298-523B-14 | Sequence 14, Appl |
| 45 | 184 | 34.5 | 589 | 15 | US-10-299-636-97 | Sequence 97, Appl |

ALIGNMENTS

RESULT 1
US-10-674-755-23
; Sequence 23, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-23

Query Match 100.0%; Score 533; DB 15; Length 108;
Best Local Similarity 100.0%; Pred. No. 4e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CLASSIFICATION: 435

3-08-710-743-24

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| Best Local Similarity | 90.7%; | Pred. No. 3.4e-35; | | |

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RESULT 5
US-09-147-875A-24
; Sequence 24, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-24

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RESULT 6
US-08-710-749-22
; Sequence 22, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-22

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Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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RESULT 7
US-08-710-749-23
; Sequence 23, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-23

Query Match      95.1%; Score 507; DB 2; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.8e-37;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 20.7935 seconds
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387.723 Million cell updates/sec

Title: US-10-674-755-23

Perfect score: 533

Sequence: 1 LEKAELENLSTLDPEGK.....TPKELDAALNELGPDGDEE 108

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 533 | 100.0 | 211 | 4 | US-08-529-055-67 |
| 4 | 533 | 100.0 | 8991 | 4 | US-08-714-741-32 |
| 5 | 511 | 95.9 | 108 | 4 | US-09-147-875A-24 |
| 6 | 507 | 95.1 | 108 | 2 | US-08-710-749-22 |
| 7 | 507 | 95.1 | 108 | 2 | US-08-710-749-23 |
| 8 | 504 | 94.6 | 212 | 4 | US-08-529-055-68 |
| 9 | 502 | 94.2 | 106 | 4 | US-09-147-875A-22 |
| 10 | 483 | 90.6 | 108 | 2 | US-08-710-749-24 |
| 11 | 483 | 90.6 | 108 | 4 | US-09-147-875A-25 |
| 12 | 483 | 90.6 | 232 | 4 | US-08-529-055-70 |
| 13 | 483 | 90.6 | 458 | 4 | US-08-529-055-73 |
| 14 | 461 | 86.5 | 108 | 2 | US-08-710-749-25 |
| 15 | 461 | 86.5 | 108 | 4 | US-09-147-875A-26 |
| 16 | 435 | 81.6 | 185 | 4 | US-08-529-055-69 |
| 17 | 329 | 61.7 | 104 | 2 | US-08-710-749-20 |
| 18 | 325 | 61.0 | 213 | 4 | US-08-529-055-47 |
| 19 | 321 | 60.2 | 104 | 4 | US-09-147-875A-21 |
| 20 | 319 | 59.8 | 104 | 2 | US-08-710-749-19 |
| 21 | 319 | 59.8 | 104 | 4 | US-09-147-875A-20 |
| 22 | 313 | 58.7 | 197 | 4 | US-08-529-055-44 |
| 23 | 313 | 58.7 | 641 | 3 | US-08-961-083-160 |
| 24 | 313 | 58.7 | 641 | 4 | US-09-536-784-160 |
| 25 | 298 | 55.9 | 102 | 2 | US-08-710-749-21 |
| 26 | 298 | 55.9 | 102 | 4 | US-09-147-875A-18 |
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| 28 | 279.5 | 52.4 | 119 | 2 | US-08-710-749-27 | Sequence 27, Appl |
| 29 | 279.5 | 52.4 | 119 | 4 | US-09-147-875A-27 | Sequence 27, Appl |
| 30 | 279.5 | 52.4 | 215 | 4 | US-08-529-055-43 | Sequence 43, Appl |
| 31 | 238 | 44.7 | 80 | 2 | US-08-710-749-18 | Sequence 18, Appl |
| 32 | 238 | 44.7 | 80 | 4 | US-09-147-875A-19 | Sequence 19, Appl |
| 33 | 211 | 39.6 | 288 | 3 | US-08-312-949-4 | Sequence 4, Appl |
| 34 | 211 | 39.6 | 288 | 3 | US-08-446-201-4 | Sequence 4, Appl |
| 35 | 211 | 39.6 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |
| 36 | 211 | 39.6 | 619 | 1 | US-08-214-164-2 | Sequence 2, Appl |
| 37 | 211 | 39.6 | 619 | 2 | US-08-467-852A-3 | Sequence 3, Appl |
| 38 | 211 | 39.6 | 619 | 2 | US-08-246-636-2 | Sequence 2, Appl |
| 39 | 211 | 39.6 | 619 | 2 | US-08-247-491A-3 | Sequence 3, Appl |
| 40 | 211 | 39.6 | 619 | 2 | US-08-319-795-2 | Sequence 2, Appl |
| 41 | 211 | 39.6 | 619 | 3 | US-08-468-985-2 | Sequence 2, Appl |
| 42 | 211 | 39.6 | 619 | 3 | US-08-312-949-2 | Sequence 2, Appl |
| 43 | 211 | 39.6 | 648 | 1 | US-08-072-070-2 | Sequence 2, Appl |
| 44 | 211 | 39.6 | 648 | 1 | US-08-469-434-2 | Sequence 2, Appl |
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ALIGNMENTS

RESULT 1
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briies, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match 100.0%; Score 533; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|---|--|----|
| Qy | 1 | LEKAELENLSTLDPEGKTQDELKAEAELELNKKVEALPNQVSELEELSKEENLK | 60 |
| Db | 1 | LEKAELENLSTLDPEGKTQDELKAEAELELNKKVEALPNQVSELEELSKEENLK | 60 |


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FT NON_TER 1 1
FT NON_TER 227 227
SQ SEQUENCE 227 AA; 24994 MW; 9D24C706228052A6 CRC64;

Query Match
 64.4%; Score 343.5; DB 2; Length 227;
Best Local Similarity 60.5%; Pred. No. 1.5e-12;
Matches 72; Conservative 16; Mismatches 20; Indels 11; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEE---AELNKKVEALPNQVSELEELSLE 56
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 LEDAELELEKVLATLDPEGKTQDELKKAEEADANIEALQNKVADLENKVAELDK 82
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 57 DNLKDAETNNVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEE 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 SDLKDAEENNVDDYKVEGLDKALTDKKVELNNTQKALDTAOKALDTALNELGPDGDEE 141
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q9L562 PRELIMINARY; PRT; 242 AA.
AC Q9L562;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=69;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=69;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=69;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF255908; AAF70098.1; -.
FT NON_TER 1 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 25843 MW; 707EA930797D2C82 CRC64;

Query Match
 62.1%; Score 331; DB 2; Length 242;
Best Local Similarity 67.6%; Pred. No. 8.2e-12;
Matches 73; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNQVSELEELSLE 60
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 LAKKQTEKLLDSDPEGKTQDELKKAEEAELDKKVEALQNKVADLEKISNLEILG 129
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 GADSD---ED-DTAALQNKLATTKAELEKTQKELDAALNELGPDGDEE 173
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q9L584 PRELIMINARY; PRT; 222 AA.
AC Q9L584;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

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OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=43;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF255543; AAF68096.1; -.
DR HSSP; P04268; 1IC2.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 23952 MW; 4824321A80C658B0 CRC64;

Query Match
 59.7%; Score 318; DB 2; Length 222;
Best Local Similarity 65.7%; Pred. No. 4.2e-11;
Matches 71; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNQVSELEELSLE 60
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 LAKKQTEKLLDSDPEGKTQDELKKAEEAELNKKVESLQNKVADLEKISNLEILG 91
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 92 GADP---ED-DTAALQNKLATTKAELEKTQKELDAALNELGPDGDEE 135
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q9L579 PRELIMINARY; PRT; 231 AA.
ID Q9L579
AC Q9L579;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=20;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=20;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF255548; AAF68101.1; -.
DR HSSP; P04268; 1IC2.
FT NON_TER 1 1
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 24990 MW; A7731F3A46460186 CRC64;

Query Match
 59.3%; Score 316; DB 2; Length 231;
Best Local Similarity 64.8%; Pred. No. 5.7e-11;
Matches 70; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEAELNKKVEALPNQVSELEELSLE 60

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OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.K., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254255; AAF68090.1; -.
FT NON_TER 1 257
SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 69.3%; Score 369.5; DB 2; Length 257;
Best Local Similarity 65.5%; Pred. No. 5.4e-14;
Matches 78; Conservative 13; Mismatches 17; Indels 11; Gaps 2;

Qy 1 LEKAEAELENLLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNQVSELEELSLE 56
Db 51 LEKAEAELENLLSTLDPEGKTQDELDEKAAEADANIEALQNKVADLENKVAELDKVETRLQ 110
Qy 57 DNLKDAETNNVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEEE 108
Db 111 SDLKDAEENNVEDYVKEGLEKALTDDKKVELNNTQKALDTAQAALDTALNELGPDGDEEE 169

RESULT 10
Q9LAX6 PRELIMINARY; PRT; 461 AA.
AC Q9LAX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6303;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071820; AAF27715.1; -.
FT NON_TER 461
SQ SEQUENCE 461 AA; 51563 MW; 249435F65585BB92 CRC64;

Query Match 66.5%; Score 354.5; DB 2; Length 461;
Best Local Similarity 62.2%; Pred. No. 7e-13;
Matches 74; Conservative 15; Mismatches 19; Indels 11; Gaps 2;

Qy 1 LEKAEAELENLLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNQVSELEELSLE 56
Db 273 LEDAELEKVLATLDPEGKTQDELDEKAAEADANIEALQNKVADLENKVAELDKVETRLQ 332
Qy 57 DNLKDAETNNVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEEE 108
Db 333 SDLKDAEENNVEDYVKEGLEKALTDDKKVELNNTQKALDTAQAALDTALNELGPDGDEEE 391

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RESULT 11
Q9LS95 PRELIMINARY; PRT; 256 AA.
AC Q9LS95;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254254; AAF68089.1; -.
FT NON_TER 1 256
SQ SEQUENCE 256 AA; 28378 MW; 650EA2D86CC523CE CRC64;

Query Match 65.0%; Score 346.5; DB 2; Length 256;
Best Local Similarity 61.3%; Pred. No. 1.1e-12;
Matches 73; Conservative 15; Mismatches 20; Indels 11; Gaps 2;

Qy 1 LEKAEAELENLLSTLDPEGKTQDELDEKAAE-----AELNKKVEALPNQVSELEELSLE 56
Db 52 LEDAELEKVLATLDPEGKTQDELDEKAAEADANIEALQNKVADLENKVAELDKVETRLQ 111
Qy 57 DNLKDAETNNVEDYIKEGLEEAIAATKQAELEKT-----PKELDAALNELGPDGDEEE 108
Db 112 SDLKDAEENNVEDYVKEGLEKALTDDKKVELNNTQKALDTAQAALDTALNELGPDGDEEE 170

RESULT 12
Q9KGS0 PRELIMINARY; PRT; 227 AA.
AC Q9KGS0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA protein (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=187;
RA Beall B.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288751; AAF91495.1; -.

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QY 1 LEKAAELENLLSTLDPGKTQDELDEKAAEALNKVKVEALPNQVSELEELSLEDNLK 60
|||
Db 295 LEKAAELENLLSTLDPGKTQDELDEKAAEALNKVKVEALQNVAELEELSLEDNLK 354
|||
QY 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
|||
Db 355 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKQDVAALNDLVDGGE 402
|||

RESULT 6
Q8GNS7 PRELIMINARY; PRT; 213 AA.
AC Q8GNS7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=128;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicunzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490268; AAN37736.1; -.
FT NON_TER 1
FT NON_TER 213
SQ SEQUENCE 213 AA; 23490 MW; 2384428409526EAB CRC64;

Query Match 90.6%; Score 483; DB 2; Length 213;
Best Local Similarity 91.7%; Pred. No. 1.4e-20;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGKTQDELDEKAAEALNKVKVEALPNQVSELEELSLEDNLK 60
|||
Db 26 LEKAAELENLLSTLDPGKTQDELDEKETAELNKVKVEALQNVAELEELSLEDNLK 85
|||
QY 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
|||
Db 86 VAETNNVEDYIKKGLUEAIAATKQAELEKTPKALDTALNELGPDGDEE 133
|||

RESULT 7
Q34097 PRELIMINARY; PRT; 653 AA.
AC Q34097;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PspA.
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF5668;
RX MEDLINE=98427139; PubMed=9746574;
RA McDaniel L.S., McDaniel D.O., Hollingshead S.K., Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
RT to the previously identified PspA sequence from strain Rxl and ability
RT of PspA from EF5668 to elicit protection against pneumococci of
RT different capsular types.";
RL Infect. Immun. 66:4748-4754(1998).
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DR EMBL; U89711; AAC62252.1; -.
DR HSSP; P06653; IHGX.
DR InterPro; IPR002479; CW binding.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR009053; Prefoldin.
DR Pfam; PF01473; CW binding 1; 9.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
SQ SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

Query Match 90.6%; Score 483; DB 2; Length 653;
Best Local Similarity 90.7%; Pred. No. 4.3e-20;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEKAAELENLLSTLDPGKTQDELDEKAAEALNKVKVEALPNQVSELEELSLEDNLK 60
|||
Db 276 LEDAELEKVLATLDPGKTQDELDEKAAEALNKVKVEALQNVAELEELSLEDNLK 335
|||
QY 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
|||
Db 336 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 383
|||

RESULT 8
Q8GNT0 PRELIMINARY; PRT; 211 AA.
AC Q8GNT0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP95;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicunzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490265; AAN37733.1; -.
FT NON_TER 1
FT NON_TER 211
SQ SEQUENCE 211 AA; 23207 MW; 096BFBE0B8CD6483 CRC64;

Query Match 69.3%; Score 369.5; DB 2; Length 211;
Best Local Similarity 65.5%; Pred. No. 4.5e-14;
Matches 78; Conservative 13; Mismatches 17; Indels 11; Gaps 2;

QY 1 LEKAAELENLLSTLDPGKTQDELDEKAAEALNKVKVEALPNQVSELEELSLEDNLK 56
|||
Db 5 LEKAAELENLLSTLDPGKTQDELDEKAAEDVNEALQNVADLENKVADLEKVEVTRLQ 64
|||
QY 57 DNLKDAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
|||
Db 65 SLDKDAEENNVYKEGLEKALTDKKVELNNLTQKALDTALNELGPDGDEE 123
|||

RESULT 9
Q9L594 PRELIMINARY; PRT; 257 AA.
AC Q9L594;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BG11703;
RX  MEDLINE=20448953; PubMed=10992499;
DOI=10.1128/IAI.68.10.5889-5900.2000;
RA  Hollingshead S.K., Becker R., Briles D.E.;
RT  "Diversity of pspA: mosaic genes and evidence for past recombination
RL  in Streptococcus pneumoniae.";
DR  EMBL; AF071821; AAF27716.1; -.
FT  HSP; P58301; 1L8D.
FT  NON_TER 481
SQ  SEQUENCE 481 AA; 53500 MW; EA3C66445EFCE2B CRC64;

Query Match          96.4%; Score 514; DB 2; Length 481;
Best Local Similarity 97.2%; Pred. No. 5.3e-22;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  1 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 60
Db  295 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 354

Qy  61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db  355 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 402

RESULT 3
Q9L5B4
ID  Q9L5B4 PRELIMINARY; PRT; 246 AA.
AC  Q9L5B4;
DT  01-OCT-2000 (TRENBLrel. 15, Created)
DT  01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE  pspA (Fragment).
GN  Name=pspA;
OS  Streptococcus pneumoniae.
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX  NCBI_TaxID=1313;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SP198;
RX  MEDLINE=20472698; PubMed=11015380;
RA  Beall B., Gherardi G., Packlam R.R., Hollingshead S.K.;
RT  "Pneumococcal pspA sequence types of prevalent multiresistant
RT  pneumococcal strains in the United States and of internationally
RL  J. Clin. Microbiol. 38:3663-3669(2000).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SP198;
RA  Beall B.W.;
RL  Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF253408; AAF67356.1; -.
DR  HSP; P05412; 1JNM.
FT  NON_TER 1
FT  NON_TER 246
SQ  SEQUENCE 246 AA; 26972 MW; 2190EED1460D26D9 CRC64;

Query Match          95.7%; Score 510; DB 2; Length 246;
Best Local Similarity 96.3%; Pred. No. 4.6e-22;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 60
Db  52 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 111

Qy  61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 108
Db  112 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 159
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RESULT 4
Q8KQK2
ID  Q8KQK2 PRELIMINARY; PRT; 107 AA.
AC  Q8KQK2;
DT  01-OCT-2002 (TRENBLrel. 22, Created)
DT  01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT  01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE  Pneumococcal surface protein A (Fragment).
GN  Name=pspA;
OS  Streptococcus pneumoniae.
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX  NCBI_TaxID=1313;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=255/00;
RX  MEDLINE=22170754; PubMed=12183557;
DOI=10.1128/IAI.70.9.5086-5090.2002;
RA  Miyaji E.N., Ferreira D.M., Lopes A.P.Y., Brandileone M.C.C.,
RA  Dias W.O., Leite L.C.C.;
RT  "Analysis of serum cross-reactivity and cross-protection elicited by
RT  immunization with DNA vaccines against Streptococcus pneumoniae
RT  expressing pspA fragments from different clades.";
RL  Infect. Immun. 70:5086-5090(2002).
DR  EMBL; AY082390; AAL92495.1; -.
FT  NON_TER 1
FT  NON_TER 107
SQ  SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

Query Match          94.7%; Score 505; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 3.8e-22;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy  1 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 60
Db  1 LEKAEAELENLLSTLDPEGKTQDELKKEAAEALNKKVEALPNQVSELEELSKELDNLIK 60

Qy  61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 107
Db  61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 107

RESULT 5
Q9LAX3
ID  Q9LAX3 PRELIMINARY; PRT; 480 AA.
AC  Q9LAX3;
DT  01-OCT-2000 (TRENBLrel. 15, Created)
DT  01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT  01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE  pspA (Fragment).
GN  Name=pspA;
OS  Streptococcus pneumoniae.
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX  Streptococcus.
OX  NCBI_TaxID=1313;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BG7561;
RX  MEDLINE=20448953; PubMed=10992499;
DOI=10.1128/IAI.68.10.5889-5900.2000;
RA  Hollingshead S.K., Becker R., Briles D.E.;
RT  "Diversity of pspA: mosaic genes and evidence for past recombination
RL  in Streptococcus pneumoniae.";
RL  Infect. Immun. 68:5889-5900(2000).
DR  EMBL; AF071824; AAF27718.1; -.
DR  InterPro; IPR000533; Tropomyosin.
DR  PRINTS; P00194; TROPOMYSIN.
FT  NON_TER 480
FT  NON_TER 480
SQ  SEQUENCE 480 AA; 53043 MW; DA013C9E0190D7A0 CRC64;

Query Match          91.7%; Score 489; DB 2; Length 480;
Best Local Similarity 92.6%; Pred. No. 1.4e-20;
Matches 100; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

| Result No. | Score | Query * | | Length | DB | ID | Description |
|------------|-------|---------|-------|--------|--------|---------------------|-------------|
| | | Match | Score | | | | |
| 1 | 514 | 96.4 | 479 | 2 | Q9LAX2 | Q9Lax2 streptococci | |
| 2 | 514 | 96.4 | 481 | 2 | Q9LAX5 | Q9Lax5 streptococci | |
| 3 | 510 | 95.7 | 246 | 2 | Q9L5B4 | Q9L5B4 streptococci | |
| 4 | 505 | 94.7 | 107 | 2 | Q8KQK2 | Q8Kqk2 streptococci | |
| 5 | 489 | 91.7 | 480 | 2 | Q9LAX3 | Q9Lax3 streptococci | |
| 6 | 483 | 90.6 | 213 | 2 | Q8GNS7 | Q8Gns7 streptococci | |
| 7 | 483 | 90.6 | 653 | 2 | Q34097 | Q34097 streptococci | |
| 8 | 369.5 | 69.3 | 211 | 2 | Q8GNT0 | Q8Gnt0 streptococci | |
| 9 | 369.5 | 69.3 | 212 | 2 | Q9L594 | Q9L594 streptococci | |
| 10 | 354.5 | 66.5 | 461 | 2 | Q9LAX6 | Q9Lax6 streptococci | |
| 11 | 346.5 | 65.0 | 256 | 2 | Q9L595 | Q9L595 streptococci | |
| 12 | 343.5 | 64.4 | 227 | 2 | Q9KGS0 | Q9Kgs0 streptococci | |
| 13 | 331 | 61.1 | 242 | 2 | Q9L562 | Q9L562 streptococci | |
| 14 | 318 | 59.7 | 222 | 2 | Q9L584 | Q9L584 streptococci | |
| 15 | 316 | 59.3 | 231 | 2 | Q9L579 | Q9L579 streptococci | |
| 16 | 316 | 59.3 | 241 | 2 | Q9L580 | Q9L580 streptococci | |
| 17 | 314 | 58.9 | 228 | 2 | Q9L5B8 | Q9L5B8 streptococci | |
| 18 | 314 | 58.9 | 235 | 2 | Q9L582 | Q9L582 streptococci | |
| 19 | 314 | 58.9 | 249 | 2 | Q9L5D4 | Q9L5d4 streptococci | |
| 20 | 314 | 58.9 | 252 | 2 | Q9L583 | Q9L583 streptococci | |
| 21 | 314 | 58.9 | 360 | 2 | Q8RKQ3 | Q8Kqk3 streptococci | |
| 22 | 314 | 58.9 | 429 | 2 | Q9LAX7 | Q9Lax7 streptococci | |
| 23 | 314 | 58.9 | 526 | 2 | Q9LAX9 | Q9Lax9 streptococci | |
| 24 | 314 | 58.9 | 608 | 2 | Q8VQ55 | Q8Vq55 streptococci | |
| 25 | 314 | 58.9 | 744 | 2 | Q97T39 | Q97t39 streptococci | |
| 26 | 312 | 58.5 | 249 | 2 | Q9L5B7 | Q9L5b7 streptococci | |
| 27 | 312 | 58.5 | 502 | 2 | Q9LAX8 | Q9Lax8 streptococci | |
| 28 | 311 | 58.3 | 249 | 2 | Q9L585 | Q9L585 streptococci | |
| 29 | 311 | 58.3 | 256 | 2 | Q9L590 | Q9L590 streptococci | |
| 30 | 304 | 57.0 | 209 | 2 | Q9L593 | Q9L593 streptococci | |
| 31 | 219 | 41.1 | 417 | 2 | Q9LAX3 | Q9Lax3 streptococci | |

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EUR. J. Biochem. 230, 1001-1006, 1995

C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59287
R:Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
Mol. Biochem. Parasitol. 58, 161-164, 1993
A>Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA from
A:Reference number: A59287; MUID:93211444; PMID:8459827
C:Accession: A59287
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1940 <WES>
A:Cross-references: UNIPROT:Q02456; GB:L01634; PIDN:AAA29905.1
A:Experimental source: strain Brazilian LE
C:Genetics:
A:Gene: MYH
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:82-752/Domain: myosin motor domain homology <WMO>

Query Match 21.6%; Score 115; DB 2; Length 1940;
Best Local Similarity 29.5%; Pred. No. 12;
Matches 49; Conservative 18; Mismatches 39; Indels 60; Gaps 8;

Qy 1 LEKAEAE---LENLLSTLDPEGTQDEL-----DK-----EAAEAE-----L 34
Db 947 LQKAEQKTKDNQRTIQSEMAQDDEMGKLNKDKKLNLEQNKRKTQEQALQAEEDKYNHL 1006
Qy 35 NKKVEALPNQVSELEELS-----KLEDNKDAETNNVEDY--IKEGLEEA 78
Db 1007 NKLKAKLESTLDEMEENLAREQKIRGVDVEKSKRLEGDLK-ATQETVDDLRLVRKRDLEE 1065
Qy 79 IATKQAE-----LEKTPKELDAALNELGPDGDEE 107
Db 1066 LRRKEAIEGGLSGKFEDEGLVAQLQKIKELQTRIQELEDLEAE 1111

RESULT 10
B75150
chromosome segregation protein (smc1) PAB2109 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75150
R:anonymous, Genoscope
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: B75150
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1177 <KAW>
A:Cross-references: UNIPROT:Q9VIR8; GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB4928
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2109
C:Superfamily: chromosome segregation protein SMC1

Query Match 21.5%; Score 114.5; DB 2; Length 1177;
Best Local Similarity 30.9%; Pred. No. 7.8;
Matches 34; Conservative 25; Mismatches 38; Indels 13; Gaps 4;

Qy 4 AEAELENLLSTLDPEGKT--QDELKEAAEAE---LNKKVEALPNQVSELEELS-----L 58
Db 387 AREFDNVVKELENARKSLYENADIKLEAEKELSRITILKAKLPICREVEKLEK 446

Qy 59 L--KDAETNNVEDYI-----KEGLEEAATKQAELEKTPKELDAALNEL 100
Db 447 LEEKKAELSNVENKISSIQRKRVKEELKNTSELQKVSSELSELEREL 496

RESULT 11
T14156
kinesin-related protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14156

R:Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
Cell 91, 357-366, 1997
A>Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome
A:Reference number: Z17893; MUID:98028574; PMID:9363944
C:Accession: T14156
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2954 <WOO>
A:Cross-references: UNIPROT:O42263; EMBL:AF027728; NID:g2586070; PIDN:g2586071; PIDN:AAC6
C:Genetics:
A:Gene: XCENP-E
C:Superfamily: centromere protein E; kinesin motor domain homology

Query Match 21.5%; Score 114.5; DB 2; Length 2954;
Best Local Similarity 29.8%; Pred. No. 20;
Matches 34; Conservative 20; Mismatches 39; Indels 21; Gaps 3;

Qy 2 EKAAEAELENLLSTLDPE---GKTODELDKAAEAEALNKKVEALPNQVSELEELS-----L 57
Db 1952 EQALNTEHRETLKSKDLALGKMEQERDEAA-----NKVIALTEKMSLEEQINENVT 2005
Qy 58 NLKDAETNNVEDYIK-----EGLEEAATKQAELEKTPKELDAALNEL 100
Db 2006 TLKEGEKEKTFYLRPFKQSSSQSSQMELESLKTKDQLQLEAEKTEISEATNEI 2059

RESULT 12
S33068
myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
N:Alternate names: surface antigen, 200K
C:Species: Schistosoma mansoni
C>Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: S33068
R:Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.
J. Immunol. 149, 3612-3620, 1992
A>Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment of
A:Reference number: A46514; MUID:93056536; PMID:1431131
A:Accession: S33068
A:Molecule type: mRNA
A:Residues: 1-527 <SOI>
A:Cross-references: UNIPROT:Q26589; EMBL:X65591
A>Note: the authors translated the codon CAA for residue 346 as Lys
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; surface antigen

Query Match 21.4%; Score 114; DB 2; Length 527;
Best Local Similarity 29.5%; Pred. No. 3.6;
Matches 49; Conservative 18; Mismatches 39; Indels 60; Gaps 8;

Qy 1 LEKAEAE---LENLLSTLDPEGTQDEL-----DK-----EAAEAE-----L 34
Db 244 LQKAEQKTKDNEIRTLQSEMAQDDEMGKLNKDKKLNLEQNKRKTQEQALQAEEDKYNHL 303
Qy 35 NKKVEALPNQVSELEELS-----KLEDNKDAETNNVEDY--IKEGLEEA 78
Db 304 NKLKAKLESTLDEMEENLAREQKIRGVDVEKSKRLEGDLK-ATQETVDDLRLVRKRDLEE 362
Qy 79 IATKQAE-----LEKTPKELDAALNELGPDGDEE 107
Db 363 LRRKEAIEGGLSGKFEDEGLVAQLQKIKELQTRIQELEDLEAE 408

RESULT 13
A47297
myosin heavy chain form B, nonmuscle - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47297; A55441
R:Bhatia-Bey, N.; Adelstein, R.S.; Dawid, I.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993
A>Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmuscul
A:Reference number: A47297; MUID:93219383; PMID:8464900
A:Accession: A47297

```

RESULT 7
Tl8296
myosin heavy chain - Entamoeba histolytica
C:Species: Entamoeba histolytica
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Tl8296
R:Guillen, N.
submitted to the EMBL Data Library, February 1997
A:Reference number: Z18865
A:Accession: Tl8296
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-2139 <GUI>
A:Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:gl1850912; PID:gl1850913; PI:
C:Genetics:
A:Gene: mhca
C:Superfamily: myosin heavy chain; myosin motor domain homology
F;91-780/Domain: myosin motor domain homology <MMO>

Query Match 21.8%; Score 116; DB 2; Length 2139;
Best Local Similarity 29.7%; Pred. No. 12; Indels 28; Gaps 6;
Matches 38; Conservative 23; Mismatches 39;

Qy 3 KAAEAELENLLS-----TLDPPGKTO-----DELDKEAAEALNKKVEALPNQVSEL 48
| | | | | : : : | | | | | : : : | | | | | : : : |
Db 2015 KYAEIEELTTEAEDALKAKWKAERKAKTSQKKLELQKTIADYE--TKEASFNTEIGKT 2072
| | | | | : : : | | | | | : : : | | | | | : : : |

Qy 49 EEELSKLEDLNKADET--NNVEDYIKEGLEEAATQKAELEKTPKELD-----AAL 97
| | | : : : | | : : : | | : : : | | : : : | | : : : |
Db 2073 QAELEKYYQOVRDETRMSSLEDEIKKG-TDALANKQLELDKYNKQVEKLKKQYKRLAA 2131
| | | | | : : : | | | | | : : : | | | | | : : : |

Qy 98 NELGPGDGD 105
Db 2132 KQSDDDSD 2139

RESULT 8
A59234
slow myosin heavy chain 3 - quail
C:Species: Coturnix coturnix
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59234
R:Nikovits Jr., W.; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, H.
J. Biol. Chem. 271, 17047-17056, 1996
A:Title: Isolation and characterization of an avian slow myosin heavy chain gene
A:Reference number: A59234; MUID:96291845; PMID:8663323
A:Accession: A59234
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1931 <NIK>
A:Cross-references: GB:U53862; NID:gl289513; PIDN:AAC59912.1; PID:gl289514
C:Superfamily: myosin heavy chain; myosin motor domain homology
F;81-761/Domain: myosin motor domain homology <MMO>

Query Match 21.6%; Score 115; DB 2; Length 1931;
Best Local Similarity 35.2%; Pred. No. 12; Indels 14; Gaps 5;
Matches 38; Conservative 21; Mismatches 35;

Qy 3 KAAEAELENLLSTLDPPGKTODELDKEAAEALNKKVEALPNQVSELEELSKLEDNI--K 60
| | | : : : | | | : : : | | | : : : | | | : : : |
Db 1021 KLEQQADDDLESSQQEKIR--MDLRARKKLGDDUKLAQESVMDLNKQQLDEERLKKK 1078
| | | : : : | | | : : : | | | : : : | | | : : : |

Qy 61 DAETNNVEDYIKEGLEEAATQKAELEKTPKELDAALNELGPDGDDEE 108
| | | : : : | | | : : : | | | : : : | | | : : : |
Db 1079 DPELNTINARIED--EQAIA---AQLQKKLELQAEIEEL-----EEE 1116
| | | : : : | | | : : : | | | : : : | | | : : : |

RESULT 9
A59287
myosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian LE)
C:Species: Schistosoma mansoni

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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71453
R;Kavrabáyasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71453
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-279 <KAW>
A;Cross-references: UNIPROT:O58021; GB:AP000001; NID:G3236128; PIDN:BA29355.1; PID:G3236128
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH0283

Query Match 23.1%; Score 123; DB 2; Length 279;
Best Local Similarity 32.8%; Pred. No. 0.52;
Matches 39; Conservative 22; Mismatches 40; Indels 18; Gaps 4;

Qy 1 LEKAELENLSTLDPGKTQDELKKEAAEAELN-----KKVEALPNQVSELEEL 52
Db 164 LEKAKGEIELKERITLEKEKELEKESVKVMEYAKAKVBELEKLEKEYEKS 223

Qy 53 SKLEDNLKDAETNNVE-DYIKEGLEEAIAATQAELE-----KTPKELDAALNELGPDG 104
Db 224 REIEGRKQVEEKIRELEEBEKGLEKINVLNENRIENLKNIGIRSAKE---ALERLLEEG 279

RESULT 5
A40997
myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)
N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Aequipecten irradians
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A40997; S13557
R;Nyitray, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Seq
A;Reference number: A40997; MUID:92011595; PMID:1917970
A;Accession: A40997
A;Molecule type: mRNA
A;Residues: 1-1938 <NYI>
A;Cross-references: UNIPROT:P24733; GB:X55714; NID:G5611; PIDN:CAA39247.1; PID:G5612
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F;86-763/Domain: myosin motor domain homology <MMOT>
F;176-183/Region: nucleotide-binding motif A (P-loop)
F;547-586/Region: actin binding #status predicted
F;653-675/Region: actin binding #status predicted
F;836-1938/Domain: coiled coil #status predicted <COI>
F;836-1276/Region: S2
F;1277-1938/Region: light meromyosin
F;182/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted

Query Match 22.6%; Score 120.5; DB 1; Length 1938;
Best Local Similarity 31.9%; Pred. No. 5.6;
Matches 53; Conservative 15; Mismatches 35; Indels 63; Gaps 9;

Qy 1 LEKAE---AELENLSTLDPGKTQDE----LDKE-AAEAELNKKV-----EAL 41
Db 958 LQAEQDKAHKDNQISTLQGEISQDEHIGKLNKEKALEANKKTSLSQAEEDKCNHL 1017

Qy 42 PNQVSELEELSLEENLK-----DAE-----TNNVEDY---IKEGLEEAI 79
Db 1018 NKLAKLEQALDELDNLEREKVGRGDSVEKAKRVEQDLKSTQENVEDLSEVRKRELEENV 1077

Qy 80 ATKQAE-----LEKTPKELDAALNELGPDGDEE 108
Db 1078 RRKEAEISSLNKLEDEQNVLVSQLRKELQARIEL-----EEE 1118

C;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:AE007317; PIDN:AAK98925.1; PID:gl
C;Genetics:
A;Gene: pspA

Query Match 39.6%; Score 211; DB 2; Length 619;
Best Local Similarity 46.8%; Pred. No. 4.4e-06;
Matches 52; Conservative 17; Mismatches 24; Indels 18; Gaps 3;

Qy 6 AELENLSTLDPGKTQDELKKE-----AAEAELNKKVEALPNQVSELE 49
Db 210 AELENQVHRLQELKEIDSESEDYAKGFRAPLQSKLDKAKKLS-KLEELSDKIDELD 268

Qy 50 EELSLEENLKDA-ETNNVEDYIKGLEEAIAATQAELEKTPKELDAALNE 99
Db 269 AEIAKLEDQLKAAEENNNVEDYFKEGLEKTTIAAKKAELEKTEADLKKAVNE 319

RESULT 3
A41971
surface protein pspA precursor - Streptococcus pneumoniae
N;Alternate names: pneumococcal surface protein A
C;Species: Streptococcus pneumoniae
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A41971; A60282; A33134
R;Yother, J.; Briles, D.E.
J. Bacteriol. 174, 601-609, 1992
A;Title: Structural properties and evolutionary relationships of PspA, a surface protein
A;Reference number: A41971; MUID:92105030; PMID:1729249
A;Accession: A41971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-619 <YOT>
A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:M74122; NID:G153840; PIDN:AAA2701
A;Note: sequence extracted from NCBI backbone (NCBIN:75635, NCBI:P:75636)
R;Talkington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.E.
Infect. Immun. 59, 1285-1289, 1991
A;Title: A 43-kilodalton pneumococcal surface protein, PspA: isolation, protective abili
A;Reference number: A60282; MUID:91169598; PMID:2004810
A;Accession: A60282
A;Molecule type: protein
A;Residues: 32-76 <TAL>
A;Experimental source: strain JV2008
C;Genetics:
A;Gene: pspA
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-619/Product: surface protein pspA #status predicted <MAT>
F;411-430/Domain: cpl repeat homology <CP01>
F;431-450/Domain: cpl repeat homology <CP02>
F;451-470/Domain: cpl repeat homology <CP03>
F;471-490/Domain: cpl repeat homology <CP04>
F;491-510/Domain: cpl repeat homology <CP05>
F;511-530/Domain: cpl repeat homology <CP06>
F;531-550/Domain: cpl repeat homology <CP07>
F;551-570/Domain: cpl repeat homology <CP08>
F;571-591/Domain: cpl repeat homology <CP09>
F;592-611/Domain: cpl repeat homology <CP10>

Query Match 39.6%; Score 211; DB 2; Length 619;
Best Local Similarity 46.8%; Pred. No. 4.4e-06;
Matches 52; Conservative 17; Mismatches 24; Indels 18; Gaps 3;

Qy 6 AELENLSTLDPGKTQDELKKE-----AAEAELNKKVEALPNQVSELE 49
Db 210 AELENQVHRLQELKEIDSESEDYAKGFRAPLQSKLDKAKKLS-KLEELSDKIDELD 268

Qy 50 EELSLEENLKDA-ETNNVEDYIKGLEEAIAATQAELEKTPKELDAALNE 99
Db 269 AEIAKLEDQLKAAEENNNVEDYFKEGLEKTTIAAKKAELEKTEADLKKAVNE 319

RESULT 4
D71453
hypothetical protein PH0283 - Pyrococcus horikoshii

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|----------------------|
| | | | | | | |
| 1 | 314 | 58.9 | 744 | 2 | P95013 | pneumococcal surface |
| 2 | 211 | 39.6 | 619 | 2 | A97887 | surface protein p |
| 3 | 211 | 39.6 | 619 | 2 | A41371 | surface protein p |
| 4 | 123 | 23.1 | 279 | 2 | D71453 | hypothetical prote |
| 5 | 120.5 | 22.6 | 1938 | 1 | A40997 | myosin heavy chain |
| 6 | 116 | 21.8 | 1961 | 1 | A61231 | myosin heavy chain |
| 7 | 116 | 21.8 | 2139 | 2 | T18296 | myosin heavy chain |
| 8 | 115 | 21.6 | 1931 | 2 | A59234 | slow myosin heavy |
| 9 | 115 | 21.6 | 1940 | 2 | A59287 | myosin heavy chain |
| 10 | 114.5 | 21.5 | 1177 | 2 | B75150 | chromosome segrega |
| 11 | 114.5 | 21.5 | 2954 | 2 | T14156 | kinesin-related pr |
| 12 | 114 | 21.4 | 527 | 2 | S33068 | myosin heavy chain |
| 13 | 114 | 21.4 | 1932 | 2 | A47297 | myosin heavy chain |
| 14 | 113.5 | 21.3 | 1964 | 2 | A59282 | nonmuscle myosin I |
| 15 | 112.5 | 21.1 | 1937 | 2 | I38055 | myosin heavy chain |
| 16 | 112 | 21.0 | 1170 | 2 | A72287 | hypothetical prote |
| 17 | 111.5 | 20.9 | 1959 | 1 | A33977 | myosin heavy chain |
| 18 | 111 | 20.8 | 281 | 2 | F75216 | hypothetical prote |
| 19 | 111 | 20.8 | 779 | 2 | C96805 | hypothetical prote |
| 20 | 110.5 | 20.7 | 399 | 2 | E71169 | hypothetical prote |
| 21 | 110 | 20.6 | 388 | 2 | A46173 | Mrp4 protein - Str |
| 22 | 109 | 20.5 | 372 | 2 | S23326 | gene M12.2 protein |
| 23 | 109 | 20.5 | 501 | 2 | A38650 | myosin heavy chain |
| 24 | 109 | 20.5 | 1976 | 2 | A59252 | myosin heavy chain |
| 25 | 108.5 | 20.4 | 1164 | 2 | T24806 | hypothetical prote |
| 26 | 108 | 20.3 | 233 | 2 | S70531 | btk2.11 protein pr |
| 27 | 108 | 20.3 | 484 | 2 | B33501 | myosin heavy chain |
| 28 | 108 | 20.3 | 1006 | 2 | C70445 | ATPase subunit of |
| 29 | 108 | 20.3 | 1269 | 2 | F84730 | probable myosin he |

```

DT 28-OCT-1997 (first entry)
XX Streptococcus pneumoniae PspA central region.
DE
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
XX bacteraemia; pneumonia.
KW
XX Streptococcus pneumoniae; strain Bg7561.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 44
FT /note= "unidentified amino acid"
XX
XX WO9709994-A1.
XX
XX 20-MAR-1997.
XX
XX 16-SEP-1996; 96WO-US014819.
XX
XX 15-SEP-1995; 95US-00529055.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
XX Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
XX
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
XX in vaccines for protecting animals against S.pneumoniae infection.
XX
XX Example 6; Fig 13; 296pp; English.
XX
XX This sequence shows the central portion, including the C-terminus of the
XX alpha-helix region and some of the proline-rich region, of pneumococcal
XX surface protein A (PspA) of Streptococcus pneumoniae strain Bg7561.
XX Comparison of the N-terminal and central regions (AAW14533-57 and
XX AAW14562-91) of PspA polypeptides from different pneumococcal strains can
XX be used to divide the strains into several families based on sequence
XX homologies. PspA polypeptides, or fragments of them, can be used in
XX vaccines to protect animals against S. pneumoniae infection and hence for
XX the prevention of diseases such as otitis media, meningitis, bacteraemia
XX and pneumonia. The sequence of the 3' half of the PspA alpha-helical
XX region and the immediate 5' tip of the coding sequence are likely to be
XX the critical sequences for predicting PspA cross-reactions and vaccine
XX composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 184 AA;
XX
XX Query Match 77.2%; Score 411.5; DB 2; Length 184;
XX Best Local Similarity 81.3%; Pred. No. 7.9e-26;
XX Matches 87; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
XX
XX QY 2 EKAAELENLSTDPGKTDDELKGAEEALNKKVEALPNQVSELEFEELSLEDNLKD 61
XX : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 KKQKVNLENLST-DPGKTDDELKGAEEALNKKVEALPNVXELEFEELSPEDNLKD 59
XX
XX QY 62 AETNNVEDYIKEGLEEAIAIKOAELEKTPKELDAALNELGPDGDEEE 108
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 60 AETHNVEDYIKFEELEAIAIKOAELEETPQEVDAALNDLVPDGGEEE 106
XX

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Search completed: November 17, 2005, 20:19:41
Job time : 76.7468 secs

```
Db      336 DAETNNVEDYIKGLEEAIAATKKALEKTKQKELDAALNELGPDGDEE 383
RESULT 13
AAW14590
ID      AAW14590 standard; protein; 233 AA.
XX
AC      AAW14590;
XX
DT      17-OCT-2003 (revised)
DT      28-OCT-1997 (first entry)
XX
DE      Streptococcus pneumoniae PspA central region.
XX
KW      PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW      bacteraemia; pneumonia.
XX
OS      Streptococcus pneumoniae; strain Ef5668.
XX
PN      WO9709994-A1.
XX
PD      20-MAR-1997.
XX
PF      16-SEP-1996; 96WO-US014819.
XX
PR      15-SEP-1995; 95US-00529055.
XX
PA      (UABR-) UAB RES FOUND.
XX
PI      Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
PI      Hollingshead S, Tart R, Brooks-Walter A;
XX      WPI; 1997-202002/18.
XX
PT      Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT      in vaccines for protecting animals against S.pneumoniae infection.
XX
PS      Example 6; Fig 13; 296pp; English.
XX
CC      This sequence shows the central portion, including the C-terminus of the
CC      alpha-helix region and some of the proline-rich region, of pneumococcal
CC      surface protein A (PspA) of Streptococcus pneumoniae strain Ef5668 (see
CC      also AAW14592). Comparison of the N-terminal and central regions
CC      (AAW14533-57 and AAW14562-91) of PspA from different pneumococcal strains
CC      can be used to divide the strains into several families based on sequence
CC      homologies. PspA polypeptides, or fragments of them, can be used in
CC      vaccines to protect animals against S. pneumoniae infection and hence for
CC      the prevention of diseases such as otitis media, meningitis, bacteraemia
CC      and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC      region and the immediate 5' tip of the coding sequence are likely to be
CC      the critical sequences for predicting PspA cross-reactions and vaccine
CC      composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ      Sequence 233 AA;
Query Match      88.6%; Score 472.5; DB 2; Length 233;
Best Local Similarity 89.9%; Pred. No. 1.1e-30;
Matches 98; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
Qy      1 LEKAAELENLLSTLDP-EGKTDQELDKAAAEALNKKVEALPNQVSELEELSKLEDNL 59
Dy      51 LEDAELEKVLATLDPEEGTKQDELDKAAAEALNKKVEALQNQVALEBELSKLEDNL 110
Qy      60 KDAETNNVEDYIKGLEEAIAATKKALEKTKPKELDAALNELGPDGDEE 108
Dy      111 KDAETNNVEDYIKGLEEAIAATKKALEKTKQKELDAALNELGPDGDEE 159
RESULT 14
ABW02623
ID      ABW02623 standard; protein; 185 AA.
XX
AC      ABW02623;
XX
DT      17-OCT-2003 (revised)
XX
DT      12-FEB-2004 (first entry)
XX
DE      Bg7561c pneumococcal surface protein A (PspA) central region.
XX
KW      Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW      immunological; gene therapy; immunostimulant.
XX
OS      Unidentified.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 45
FT      /label= Unknown
XX
PN      US6592876-B1.
XX
PD      15-JUL-2003.
XX
PF      15-SEP-1995; 95US-00529055.
XX
PR      20-APR-1993; 93US-00048896.
XX
PR      06-JUN-1995; 95US-00465746.
XX
PA      (UABR-) UAB RES FOUND.
XX
PI      Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX      WPI; 2003-862841/80.
XX
PT      Immunological composition for obtaining expression products used for
PT      detecting the presence of Streptococcus pneumoniae or its strain,
PT      comprises at least two different full length isolated gene encoding
PT      pneumococcal surface protein A.
XX
PS      Example 6; SEQ ID NO 69; 121pp; English.
XX
CC      The present invention relates to an immunological composition comprising
CC      at least 2 different full length isolated genes encoding pneumococcal
CC      surface protein A (PspAs) from different groups based on restriction
CC      fragment polymorphism analysis. The invention is useful for obtaining
CC      expression products by recombinant techniques to detect, determine,
CC      isolate or diagnose the presence of Streptococcus pneumoniae or its
CC      strain. The expression product is useful for preparing antigenic,
CC      immunological or vaccine compositions, for eliciting antibodies, an
CC      immunological response (other than or additional to antibodies) or a
CC      protective response (including antibody or other immunological response
CC      by administering compositions to a host). The invention is also useful as
CC      vaccines and in gene therapy. The present sequence is Bg7561c
CC      pneumococcal surface protein A (PspA) central region. This sequence is
CC      used in the exemplification of the invention
XX
SQ      Sequence 185 AA;
Query Match      81.6%; Score 435; DB 7; Length 185;
Best Local Similarity 83.2%; Pred. No. 9.6e-28;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
Qy      2 EKAAELENLLSTLDPGKTKQDELDKAAAEALNKKVEALPNQVSELEELSKLEDNLKD 61
Dy      1 KKQKNLENLLSTLDPGKTKQDELDKAAAEALNKKVEALPNPYXLEELSELPEDNLKD 60
Qy      62 AETNNVEDYIKGLEEAIAATKKALEKTKPKELDAALNELGPDGDEE 108
Dy      61 AETNNVEDYIKGLEEAIAATKKALEKTKPQEVDAALNDLVPDGGEE 107
RESULT 15
AAW14589
ID      AAW14589 standard; protein; 184 AA.
XX
XX      AAW14589;
AC      AAW14589;
XX
DT      17-OCT-2003 (revised)
```


DR WPI; 2004-192068/18.
XX Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.
XX Claim 17; SEQ ID NO 2; 41pp; English.
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rx1 strain of Streptococcus
CC pneumoniae.
XX Sequence 369 AA;
SQ
Query Match 90.6%; Score 483; DB 8; Length 369;
Best Local Similarity 90.7%; Pred. No. 2.6e-31;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LEKAAELENLSTLDPSGKTQDELDEKAAEALNKVEALPNQVSEEEESKLEDNLK 60
Db 245 LEDAELEKVLATLDPSGKTQDELDEKAAEALNKVEALQNVAELEEEESKLEDNLK 304
QY 61 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE 108
Db 305 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE 352
RESULT 9
AAW14592
ID AAW14592 standard; protein; 458 AA.
AC AAW14592;
XX 17-OCT-2003 (revised)
DT 27-OCT-1997 (first entry)
XX Streptococcus pneumoniae PspA surface protein.
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX Streptococcus pneumoniae; strain Ef5668.
OS
XX WO9709994-A1.
XX 20-MAR-1997.
PD
XX 16-SEP-1996; 96WO-US014819.
PF
XX 15-SEP-1995; 95US-00529055.
PR (UABR-) UAB RES FOUND.
XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX WPI; 1997-202002/18.
DR N-PSDB; AAT61724.
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX Disclosure; Fig 13; 296pp; English.
XX This sequence comprises the pneumococcal surface protein A (pspA) of
CC Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the

CC pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be
CC used in vaccines to protect animals against S. pneumoniae infection and
CC hence for the prevention of diseases such as otitis media, meningitis,
CC bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 458 AA;
Query Match 90.6%; Score 483; DB 2; Length 458;
Best Local Similarity 90.7%; Pred. No. 3.3e-31;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 LEKAAELENLSTLDPSGKTQDELDEKAAEALNKVEALPNQVSEEEESKLEDNLK 60
Db 276 LEDAELEKVLATLDPSGKTQDELDEKAAEALNKVEALQNVAELEEEESKLEDNLK 335
QY 61 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE 108
Db 336 DAETNNVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELGPDGDEE 383
RESULT 10
ABW02626
ID ABW02626 standard; protein; 458 AA.
XX
AC ABW02626;
XX 12-FEB-2004 (first entry)
DT
XX Ef5668 pneumococcal surface protein A (PspA).
DE
XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX Unidentified.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 458
FT /note= "Encoded by GC"
XX
XX US6592876-B1.
PD 15-JUL-2003.
XX
PF 15-SEP-1995; 95US-00529055.
XX
PR 20-APR-1993; 93US-00048896.
PR 06-JUN-1995; 95US-00465746.
XX
PA (UABR-) UAB RES FOUND.
XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
PI WPI; 2003-862841/80.
DR N-PSDB; AAD64535.
XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
XX pneumococcal surface protein A.
PS Example 6; SEQ ID NO 73; 121pp; English.
XX The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAs) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antigenic,
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response

XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
 KW immunological; gene therapy; immunostimulant.
 XX
 OS Unidentified.
 XX
 PN US5592876-B1.
 XX
 PD 15-JUL-2003.
 XX
 XX 15-SEP-1995; 95US-00529055.
 XX
 XX 20-APR-1993; 93US-00048896.
 PR 06-JUN-1995; 95US-00465746.
 XX
 XX (UABR-) UAB RES FOUND.
 PA
 XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
 PI WPI; 2003-862841/80.
 DR
 XX Immunological composition for obtaining expression products used for
 PT detecting the presence of Streptococcus pneumoniae or its strain,
 PT comprises at least two different full length isolated gene encoding
 PT pneumococcal surface protein A.
 XX
 XX Example 6; SEQ ID NO 70; 121pp; English.
 PS
 XX The present invention relates to an immunological composition comprising
 XX at least 2 different full length isolated genes encoding pneumococcal
 CC surface protein A (PspA) from different groups based on restriction
 CC fragment polymorphism analysis. The invention is useful for obtaining
 CC expression products by recombinant techniques to detect, determine,
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its
 CC strain. The expression product is useful for preparing antigenic,
 CC immunological or vaccine compositions, for eliciting antibodies, an
 CC immunological response (other than or additional to antibodies) or a
 CC protective response (including antibody or other immunological response
 CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is Ef5668c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention
 XX
 XX Sequence 232 AA;
 SQ

Query Match 90.6%; Score 483; DB 7; Length 232;
 Best Local Similarity 90.7%; Pred. No. 1.5e-31;
 Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSEBELSKLEDNLK 60
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 51 LEDAELEKVLATLDPEGKTQDELKAAAEALNKKVEALQNVAELEBELSKLEDNLK 110
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKGLEEAATKQAELEKTPKELDAALNELGPDGDEE 108
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 111 DAETNNVEDYIKGLEEAATKQAELEKTPKELDAALNELGPDGDEE 158
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
 AD052055
 ID AD052055 standard; protein; 275 AA.
 XX
 AC AD052055;
 XX
 XX 12-AUG-2004 (first entry)
 DT
 XX S. pneumoniae strain EF5688 PspA alpha helical domain.
 DE
 XX Immunogenic composition; vaccine; Th2-type immune response;
 KW pneumococcal surface protein A; PspA.
 XX
 XX Streptococcus pneumoniae.
 OS

PN US2004101531-A1.
 XX
 PD 27-MAY-2004.
 XX
 XX 15-APR-2003; 2003US-00414532.
 XX
 PR 16-APR-2002; 2002US-0372710P.
 XX
 XX (CURT/) CURTISS R.
 PA (KANG/) KANG H Y.
 XX
 XX Curtiss R, Kang HY;
 PI WPI; 2004-399655/37.
 XX
 XX New vaccine comprising a live attenuated strain of pathogenic gram-
 PT negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 PT or bacteria.
 XX
 PS Claim 17; SEQ ID NO 1; 94pp; English.
 XX
 XX The invention relates to immunogenic compositions and vaccines comprising
 CC a live attenuated strain of pathogenic gram negative bacteria that
 CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
 CC response in a vertebrate against pathogens, e.g., helminths, fungi,
 CC viruses, protozoans or bacteria. The present sequence is Streptococcus
 CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
 CC helical domain. This sequence is used in the invention.
 XX
 XX Sequence 275 AA;
 SQ

Query Match 90.6%; Score 483; DB 8; Length 275;
 Best Local Similarity 90.7%; Pred. No. 1.8e-31;
 Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSEBELSKLEDNLK 60
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 167 LEDAELEKVLATLDPEGKTQDELKAAAEALNKKVEALQNVAELEBELSKLEDNLK 226
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 DAETNNVEDYIKGLEEAATKQAELEKTPKELDAALNELGPDGDEE 108
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 227 DAETNNVEDYIKGLEEAATKQAELEKTPKELDAALNELGPDGDEE 274
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
 ADK52496
 ID ADK52496 standard; protein; 369 AA.
 XX
 AC ADK52496;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 XX alpha helical region PspA molecule from the Rx1 strain.
 DE
 XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
 KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
 KW Hodgkin's disease.
 XX
 OS Streptococcus pneumoniae.
 XX
 XX WO2004016231-A2.
 PN
 XX 26-FEB-2004.
 PD
 XX 17-FEB-2003; 2003WO-US008199.
 PF
 XX 15-MAR-2002; 2002US-0365351P.
 PR
 XX (UABR-) UAB RES FOUND.
 PA
 XX Briles DE;
 PI
 XX

ID ABW02622 standard; protein; 212 AA.

DE Ef5668c pneumococcal surface protein A (PspA) central region.

CC vaccines and in gene therapy. The present sequence is Bg11703c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention
 XX
 SQ Sequence 211 AA;

Query Match 100.0%; Score 533; DB 7; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 60
 Db 25 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 84

Qy 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 85 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 132

RESULT 2
 AA14587
 ID AA14587 standard; protein; 238 AA.
 AC AA14587;
 XX
 DT 17-OCT-2003 (revised)
 DT 28-OCT-1997 (first entry)
 XX Streptococcus pneumoniae PspA central region.
 DE
 XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
 KW bacteraemia; pneumonia.
 XX Streptococcus pneumoniae; strain Bg11703.
 OS
 XX WO9709994-A1.
 PN
 XX 20-MAR-1997.
 PD
 XX 16-SEP-1996; 96WO-US014819.
 PF
 XX 15-SEP-1995; 95US-00529055.
 PR
 XX (UABR-) UAB RES FOUND.
 PA
 XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 PI
 XX WPI; 1997-202002/18.
 DR
 XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
 PT in vaccines for protecting animals against S.pneumoniae infection.
 PT
 XX Example 6; Fig 13; 296pp; English.

CC This sequence shows the central portion, including the C-terminus of the
 CC alpha-helix region and some of the proline-rich region, of pneumococcal
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg11703.
 CC Comparison of the N-terminal and central regions (AA14533-57 and
 CC AA14562-91) of PspA polypeptides from different pneumococcal strains can
 CC be used to divide the strains into several families based on sequence
 CC homologies. PspA polypeptides, or fragments of them, can be used in
 CC vaccines to protect animals against S. pneumoniae infection and hence for
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
 CC region and the immediate 5' tip of the coding sequence are likely to be
 CC the critical sequences for predicting PspA cross-reactions and vaccine
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 533; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 60
 Db 25 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 84

Qy 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 108
 Db 85 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 132

RESULT 3
 ABU08487
 ID ABU08487 standard; protein; 8991 AA.
 XX
 AC ABU08487;
 XX
 DT 24-JUN-2003 (first entry)
 DT
 XX S. pneumoniae pneumococcal surface protein A (PspA) protein.
 DE
 XX Pneumococcal surface protein C; PspC; pneumococcal surface protein A;
 KW alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;
 KW antibacterial.
 XX Streptococcus pneumoniae.
 OS
 XX Key Location/Qualifiers
 PH Misc-difference 1..8991
 FT /note= "All Xaa residues within this sequence are
 FT unknown"
 FT
 XX US6500613-B1.
 PN
 XX 31-DEC-2002.
 PD
 XX 16-SEP-1996; 96US-00714741.
 PF
 XX 15-SEP-1995; 95US-00529055.
 PR
 XX (UYAL-) UNIV ALABAMA.
 PA
 XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 PI
 XX WPI; 2003-361534/34.
 DR
 XX Isolated PspC amino acid sequence used as polymerase chain reaction or
 PT hybridization probe, comprises pneumococcal surface protein having alpha-
 PT helical, proline rich and repeat regions.
 PT
 XX Disclosure; Col 145-188; 186pp; English.
 PS
 XX The present invention relates to the isolation of Streptococcus
 CC pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide
 CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA) -
 CC like protein having alpha-helical, proline rich and repeat regions. The
 CC PspC and PspA proteins may be used in a vaccine to protect against
 CC pneumococcal infections. The polynucleotide sequences encoding PspC and
 CC PspA may be used for the expression of the proteins, and as PCR primers
 CC or hybridisation probes. The present sequence represents S. pneumoniae
 CC PspA protein
 XX
 SQ Sequence 8991 AA;

Query Match 100.0%; Score 533; DB 6; Length 8991;
 Best Local Similarity 100.0%; Pred. No. 7.9e-34;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 60
 Db 7981 LEKAAELENLSTLDPEGKTQDELKAAAEALNKKVEALPNQVSELEELSKEIDNLK 8040

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 76.7468 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-23
Perfect score: 533
Sequence: 1 LEKAEAELENLSTLDEPGK.....TPKELDAALNELGPDGDEEE 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 533 | 100.0 | 211 | 7 | ABW02621 Bg11703c |
| 2 | 533 | 100.0 | 238 | 2 | AAW14587 Streptoco |
| 3 | 533 | 100.0 | 8991 | 6 | ABU08487 S. pneumo |
| 4 | 504 | 94.6 | 212 | 2 | AAW14588 Streptoco |
| 5 | 504 | 94.6 | 212 | 7 | ABW02622 |
| 6 | 483 | 90.6 | 232 | 7 | ABW02624 Ef5668c p |
| 7 | 483 | 90.6 | 275 | 8 | ADO52055 S. pneumo |
| 8 | 483 | 90.6 | 369 | 8 | ADK52496 alpha hel |
| 9 | 483 | 90.6 | 458 | 2 | AAW14592 Streptoco |
| 10 | 483 | 90.6 | 458 | 7 | ABW02626 |
| 11 | 483 | 90.6 | 653 | 8 | ADK52495 PspA mole |
| 12 | 483 | 90.6 | 653 | 8 | ADO52080 S. pneumo |
| 13 | 472.5 | 88.6 | 233 | 2 | AAW14590 Streptoco |
| 14 | 435 | 81.6 | 185 | 7 | ABW02623 Bg7561c p |
| 15 | 411.5 | 77.2 | 184 | 2 | AAW14589 Streptoco |
| 16 | 325 | 61.0 | 213 | 7 | ABW02601 Bg8090c p |
| 17 | 322.5 | 60.5 | 459 | 8 | ADO15316 |
| 18 | 314 | 58.9 | 213 | 2 | AAW14567 Streptoco |
| 19 | 314 | 58.9 | 426 | 8 | ADK52498 alpha hel |
| 20 | 314 | 58.9 | 526 | 8 | ADK52497 PspA mole |
| 21 | 314 | 58.9 | 744 | 6 | ABU00449 S. pneumo |
| 22 | 314 | 58.9 | 744 | 8 | ADM92054 S. pneumo |
| 23 | 314 | 58.9 | 745 | 3 | AAW14652 Streptoco |
| 24 | 313 | 58.7 | 197 | 7 | ABW02598 Ac122c pn |
| 25 | 313 | 58.7 | 641 | 2 | AAW61217 Streptoco |

ALIGNMENTS

RESULT 1

ABW02621
ID ABW02621 standard; protein; 211 AA.

XX AC ABW02621;

XX DT 12-FEB-2004 (first entry)

XX DE Bg11703c pneumococcal surface protein A (PspA) central region.

XX KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
immunological; gene therapy; immunostimulant.

XX OS Unidentified.

XX FN US6592876-B1.

XX PD 15-JUL-2003.

XX PF 15-SEP-1995; 95US-00529055.

XX PR 20-APR-1993; 93US-00048896.

XX PR 06-JUN-1995; 95US-00465746.

XX (UABR-) UAB RES FOUND.

XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX WPI; 2003-862841/80.

Immunological composition for obtaining expression products used for detecting the presence of Streptococcus pneumoniae or its strain, comprises at least two different full length isolated gene encoding pneumococcal surface protein A.

Example 6; SEQ ID NO 67; 121pp; English.

The present invention relates to an immunological composition comprising at least 2 different full length isolated genes encoding pneumococcal surface protein A (PspAs) from different groups based on restriction fragment polymorphism analysis. The invention is useful for obtaining expression products by recombinant techniques to detect, determine, isolate or diagnose the presence of Streptococcus pneumoniae or its strain. The expression product is useful for preparing antigenic, immunological or vaccine compositions, for eliciting antibodies, an immunological response (other than or additional to antibodies), or a protective response (including antibody or other immunological response by administering compositions to a host). The invention is also useful as

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; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa at position 2 is unknown
US-10-299-636-62

Query Match          60.2%; Score 315; DB 15; Length 213;
Best Local Similarity 64.5%; Pred. No. 4.2e-17;
Matches 69; Conservative 11; Mismatches 23; Indels 4; Gaps 2;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59
Db 59 LAKQTELEKLLDNLDPGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59

QY 60 DAETNVEDYIKGLEEAEATKQAELEKTPKELDAALNELGPDGDEE 106
Db 119 GADPEDD---TAAALPNKLATKKAEEFKTPKELDAALNELGPDGDEE 162

RESULT 14
US-10-674-755-21
; Sequence 21, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-21

Query Match          59.5%; Score 311; DB 15; Length 104;
Best Local Similarity 64.5%; Pred. No. 3.7e-17;
Matches 69; Conservative 11; Mismatches 23; Indels 4; Gaps 2;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59
Db 1 LAKQTELEKLLDNLDPGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 60

QY 60 DAETNVEDYIKGLEEAEATKQAELEKTPKELDAALNELGPDGDEE 106
Db 61 GADPEDD---TAAALPNKLATKKAEEFKTPKELDAALNELGPDGDEE 104

RESULT 15
US-10-674-755-20
; Sequence 20, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-20

Query Match          59.1%; Score 309; DB 15; Length 104;
Best Local Similarity 63.6%; Pred. No. 5.4e-17;
Matches 68; Conservative 13; Mismatches 22; Indels 4; Gaps 2;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59
Db 1 LAKQTELEKLLDNLDPGKTQDELDKAAEAEALNKKVEALPNQV-ELEEEELSKLEDNLK 60

QY 60 DAETNVEDYIKGLEEAEATKQAELEKTPKELDAALNELGPDGDEE 106
Db 61 GADSEDD---TAAALPNKLATKKAEEFKTPKELDAALNELGPDGDEE 104

Search completed: November 17, 2005, 20:29:17
Job time : 70.5017 secs
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Qy 1 LEKAAELENLLSTLDPGKTQDELKGAABAEALNKKVEALPNQV-ELEELSKEEDNLK 59
 Db 276 LEDAELEKVLATLDPGKTQDELKGAABAEALNKKVEALQNVAELEELSKEEDNLK 335
 Qy 60 DAETN-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 Db 336 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 383

RESULT 10
 US-10-414-532-26
 ; Sequence 26, Application US/10414532
 ; Publication No. US20040101531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CURTISS III, ROY
 ; APPLICANT: KANG, HO YOUNG
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
 ; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
 ; FILE REFERENCE: 56029-40437
 ; CURRENT APPLICATION NUMBER: US/10/414,532
 ; PRIOR FILING DATE: 2003-04-15
 ; PRIOR APPLICATION NUMBER: 60/372,710
 ; PRIOR FILING DATE: 2002-04-16
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 26
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-10-414-532-26

Query Match 87.0%; Score 455; DB 16; Length 653;
 Best Local Similarity 89.8%; Pred. No. 1.5e-27;
 Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPGKTQDELKGAABAEALNKKVEALPNQV-ELEELSKEEDNLK 59
 Db 276 LEDAELEKVLATLDPGKTQDELKGAABAEALNKKVEALQNVAELEELSKEEDNLK 335
 Qy 60 DAETN-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 Db 336 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 383

RESULT 11
 US-10-674-755-26
 ; Sequence 26, Application US/10674755
 ; Publication No. US20040067237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BECKER et al.
 ; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
 ; FILE REFERENCE: 454312-2471
 ; CURRENT APPLICATION NUMBER: US/10/674,755
 ; CURRENT FILING DATE: 2003-09-30
 ; PRIOR APPLICATION NUMBER: US/09/147,875A
 ; PRIOR FILING DATE: 1999-05-24
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 26
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (1)..(108)
 ; OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
 US-10-674-755-26

Query Match 83.9%; Score 439; DB 15; Length 108;
 Best Local Similarity 88.0%; Pred. No. 3.4e-27;
 Matches 95; Conservative 4; Mismatches 7; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPGKTQDELKGAABAEALNKKVEALPNQV-ELEELSKEEDNLK 59

Db 1 LEKAAELENLLSTLDPGKTQDELKGAABAEALNKKVEALPNVXLEELSPPEDNLK 60
 Qy 60 DAETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGDEE 108

RESULT 12
 US-10-299-636-84
 ; Sequence 84, Application US/10299636
 ; Publication No. US20040077847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briles, David E
 ; APPLICANT: McDaniel, Larry S
 ; APPLICANT: Swiatlo, Edwin
 ; APPLICANT: Yotter, Janet
 ; APPLICANT: Crain, Marilyn J
 ; APPLICANT: Hollingshead, Susan
 ; APPLICANT: Tart, Rebecca
 ; APPLICANT: Brooke-Walter, Alexis
 ; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 57909/361
 ; CURRENT APPLICATION NUMBER: US/10/299,636
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: 08/714,741
 ; PRIOR FILING DATE: 1996-09-16
 ; PRIOR APPLICATION NUMBER: 08/529,055
 ; PRIOR FILING DATE: 1995-09-15
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 84
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (45)
 ; OTHER INFORMATION: Xaa at position 45 is unknown
 US-10-299-636-84

Query Match 79.0%; Score 413; DB 15; Length 185;
 Best Local Similarity 83.2%; Pred. No. 7e-25;
 Matches 89; Conservative 6; Mismatches 10; Indels 2; Gaps 2;
 Qy 2 EKAAELENLLSTLDPGKTQDELKGAABAEALNKKVEALPNQV-ELEELSKEEDNLK 60
 Db 1 KKQVNLLENLLSTLDPGKTQDELKGAABAEALNKKVEALPNVXLEELSPPEDNLK 60
 Qy 61 AETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 Db 61 AETNNVEDYIKEGLEEAIAATKQAELEETPOEVDAAALNDLVPDGGDEE 107

RESULT 13
 US-10-299-636-62
 ; Sequence 62, Application US/10299636
 ; Publication No. US20040077847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briles, David E
 ; APPLICANT: McDaniel, Larry S
 ; APPLICANT: Swiatlo, Edwin
 ; APPLICANT: Yotter, Janet
 ; APPLICANT: Crain, Marilyn J
 ; APPLICANT: Hollingshead, Susan
 ; APPLICANT: Tart, Rebecca
 ; APPLICANT: Brooke-Walter, Alexis
 ; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 57909/361
 ; CURRENT APPLICATION NUMBER: US/10/299,636
 ; CURRENT FILING DATE: 2002-11-19
 ; PRIOR APPLICATION NUMBER: 08/714,741
 ; PRIOR FILING DATE: 1996-09-16

Db 88 DAETNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 135

RESULT 6

US-10-674-755-25
; Sequence 25, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1993-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-25

Query Match 87.0%; Score 455; DB 15; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.9e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEALNKKVEALPNQV-ELEEELSKLEDNLK 59

Db 1 LEDAELEKVLATLDPEGKTQDELKKAEEALNKKVEALQNVAAELEEELSKLEDNLK 60

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106

Db 61 DAETNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 7

US-10-299-636-85
; Sequence 85, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-85

Query Match 87.0%; Score 455; DB 15; Length 232;
Best Local Similarity 89.8%; Pred. No. 4.5e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEALNKKVEALPNQV-ELEEELSKLEDNLK 59

Db 51 LEDAELEKVLATLDPEGKTQDELKKAEEALNKKVEALQNVAAELEEELSKLEDNLK 110

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 111 DAETNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 158

RESULT 8

US-10-414-532-1
; Sequence 1, Application US/10414532
; Publication No. US20040101531A1
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-414-532-1

Query Match 87.0%; Score 455; DB 16; Length 275;
Best Local Similarity 89.8%; Pred. No. 5.5e-28;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAAELENLSTLDPEGKTQDELKKAEEALNKKVEALPNQV-ELEEELSKLEDNLK 59

Db 167 LEDAELEKVLATLDPEGKTQDELKKAEEALNKKVEALQNVAAELEEELSKLEDNLK 226

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106

Db 227 DAETNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 274

RESULT 9

US-10-299-636-88
; Sequence 88, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-88

Query Match 87.0%; Score 455; DB 15; Length 458;
Best Local Similarity 89.8%; Pred. No. 1e-27;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

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US-10-674-755-23
; Sequence 23, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-23

Query Match          96.0%; Score 502; DB 15; Length 108;
Best Local Similarity 98.1%; Pred. No. 3.8e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEELSKELDNLK 59
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSKELDNLK 60

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 3
US-10-299-636-82
; Sequence 82, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-82

Query Match          96.0%; Score 502; DB 15; Length 211;
Best Local Similarity 98.1%; Pred. No. 8.2e-32;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEELSKELDNLK 59
Db 25 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVSELEELSKELDNLK 84

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 85 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 132
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```
RESULT 4
US-10-674-755-24
; Sequence 24, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-24

Query Match          93.3%; Score 488; DB 15; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.7e-31;
Matches 104; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEELSKELDNLK 59
Db 1 LEKAGAGLELLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVAELEELSKELDNLK 60

Qy 60 DAETN-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 5
US-10-299-636-83
; Sequence 83, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E
; APPLICANT: McDaniel, Larry S
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
; FILE REFERENCE: 57909/361
; CURRENT APPLICATION NUMBER: US/10/299,636
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 08/714,741
; PRIOR FILING DATE: 1996-09-16
; PRIOR APPLICATION NUMBER: 08/529,055
; PRIOR FILING DATE: 1995-09-15
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-299-636-83

Query Match          92.0%; Score 481; DB 15; Length 212;
Best Local Similarity 95.4%; Pred. No. 3.7e-30;
Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Db 28 LEKAGAGLELLSTLDPEGKTQDELDKAAAEALNKKVEALPNQVAELEELSKELDNLK 87

Qy 60 DAETN-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 108
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:29:52 ; Search time 70.5017 Seconds
(without alignments)
629.082 Million cell updates/sec

Title: US-10-674-755-22
Perfect score: 523
Sequence: 1 LEKAEAELENLSTLDPEKG.....TPKELDAALNELGPDGDEE 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues
Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|-------------------|-------|-------------|--------|----|------------------|
| 1 | 523 | 100.0 | 106 | 15 | US-10-674-755-22 |
| 2 | 502 | 96.0 | 108 | 15 | US-10-674-755-23 |
| 3 | 502 | 96.0 | 211 | 15 | US-10-299-636-82 |
| 4 | 488 | 93.3 | 108 | 15 | US-10-674-755-24 |
| 5 | 481 | 92.0 | 212 | 15 | US-10-299-636-83 |
| 6 | 455 | 87.0 | 108 | 15 | US-10-674-755-25 |
| 7 | 455 | 87.0 | 232 | 15 | US-10-299-636-85 |
| 8 | 455 | 87.0 | 275 | 16 | US-10-414-532-1 |
| 9 | 455 | 87.0 | 458 | 15 | US-10-299-636-88 |
| 10 | 455 | 87.0 | 653 | 16 | US-10-414-532-26 |
| 11 | 439 | 83.9 | 108 | 15 | US-10-674-755-26 |
| Sequence 22, Appl | | | | | |
| Sequence 23, Appl | | | | | |
| Sequence 82, Appl | | | | | |
| Sequence 24, Appl | | | | | |
| Sequence 83, Appl | | | | | |
| Sequence 25, Appl | | | | | |
| Sequence 85, Appl | | | | | |
| Sequence 1, Appl | | | | | |
| Sequence 86, Appl | | | | | |
| Sequence 26, Appl | | | | | |

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|----|-------|------|-----|----|----------------------|--------------------|
| 12 | 413 | 79.0 | 185 | 15 | US-10-299-636-84 | Sequence 84, Appl |
| 13 | 315 | 60.2 | 213 | 15 | US-10-299-636-62 | Sequence 62, Appl |
| 14 | 311 | 59.5 | 104 | 15 | US-10-674-755-21 | Sequence 21, Appl |
| 15 | 309 | 59.1 | 104 | 15 | US-10-674-755-20 | Sequence 20, Appl |
| 16 | 304 | 58.1 | 744 | 10 | US-09-769-787-184 | Sequence 184, Appl |
| 17 | 304 | 58.1 | 744 | 17 | US-10-472-528-32 | Sequence 32, Appl |
| 18 | 303 | 57.9 | 641 | 9 | US-09-765-272-160 | Sequence 160, Appl |
| 19 | 303 | 57.9 | 641 | 20 | US-11-106-649-160 | Sequence 160, Appl |
| 20 | 300 | 57.4 | 197 | 15 | US-10-299-636-59 | Sequence 59, Appl |
| 21 | 296.5 | 56.7 | 459 | 15 | US-10-702-305A-18 | Sequence 18, Appl |
| 22 | 288 | 55.1 | 102 | 15 | US-10-674-755-18 | Sequence 18, Appl |
| 23 | 275 | 52.6 | 233 | 15 | US-10-299-636-67 | Sequence 67, Appl |
| 24 | 272 | 52.0 | 487 | 16 | US-10-414-532-34 | Sequence 34, Appl |
| 25 | 272 | 52.0 | 487 | 16 | US-10-414-532-31 | Sequence 21, Appl |
| 26 | 272 | 52.0 | 524 | 16 | US-10-414-532-28 | Sequence 28, Appl |
| 27 | 262.5 | 50.2 | 290 | 16 | US-10-414-532-65 | Sequence 65, Appl |
| 28 | 260.5 | 49.8 | 230 | 16 | US-10-414-532-32 | Sequence 32, Appl |
| 29 | 260.5 | 49.8 | 230 | 16 | US-10-414-533-19 | Sequence 19, Appl |
| 30 | 257.5 | 49.2 | 119 | 15 | US-10-674-755-27 | Sequence 27, Appl |
| 31 | 257.5 | 49.2 | 215 | 15 | US-10-299-636-58 | Sequence 58, Appl |
| 32 | 225 | 43.0 | 80 | 15 | US-10-674-755-19 | Sequence 19, Appl |
| 33 | 194 | 37.1 | 354 | 15 | US-10-299-636-105 | Sequence 105, Appl |
| 34 | 194 | 37.1 | 588 | 15 | US-10-299-636-96 | Sequence 96, Appl |
| 35 | 194 | 37.1 | 619 | 10 | US-09-882-774-1 | Sequence 1, Appl |
| 36 | 194 | 37.1 | 619 | 15 | US-10-282-122A-73702 | Sequence 73702, A |
| 37 | 194 | 37.1 | 619 | 16 | US-10-414-532-72 | Sequence 72, Appl |
| 38 | 182 | 34.8 | 204 | 15 | US-10-299-636-66 | Sequence 66, Appl |
| 39 | 178 | 34.0 | 99 | 15 | US-10-674-755-11 | Sequence 11, Appl |
| 40 | 173 | 33.1 | 198 | 15 | US-10-299-636-76 | Sequence 76, Appl |
| 41 | 169.5 | 32.4 | 100 | 15 | US-10-674-755-12 | Sequence 12, Appl |
| 42 | 167 | 31.9 | 141 | 14 | US-10-254-995-2 | Sequence 2, Appl |
| 43 | 167 | 31.9 | 589 | 9 | US-09-748-875-14 | Sequence 14, Appl |
| 44 | 167 | 31.9 | 589 | 10 | US-09-298-523B-14 | Sequence 14, Appl |
| 45 | 167 | 31.9 | 589 | 15 | US-10-299-636-97 | Sequence 97, Appl |

ALIGNMENTS

RESULT 1
US-10-674-755-22
; Sequence 22, Application US/10674755
; Publication No. US20040067237A1
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/10/674,755
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/147,875A
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-674-755-22

Query Match 100.0%; Score 523; DB 15; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.2e-34;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | LEKAEAELENLSTLDPEGKTQDELKAEAELENKKVEALPNQVLEFEELSKLDNLKD | 60 |
| Qy | 61 | AETNVEDIKESGLEEATKQAELEKTPKELDAALNELGPDGDEE | 106 |
| Db | 61 | AETNVEDIKESGLEEATKQAELEKTPKELDAALNELGPDGDEE | 106 |

RESULT 2

MOLECULE TYPE: peptide
US-08-529-055-73

Query Match 87.0%; Score 455; DB 4; Length 458;
Best Local Similarity 89.8%; Pred. No. 1.4e-32;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
Db 276 LEAAELEKVLATLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 335
Qy 60 DAETNVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 106
Db 336 DAETNNVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 383

RESULT 14

US-08-710-749-25
Sequence 25, Application US/08710749
Patent No. 5955089
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Hollingshead, Susan
APPLICANT: Becker, Robert
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-25

Query Match 83.9%; Score 439; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 6.3e-32;
Matches 95; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNVXELEELSPPEIDLK 60
Qy 60 DAETNVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNHVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 108

RESULT 15

US-09-147-875A-26
Sequence 26, Application US/09147875A
Patent No. 6638516
GENERAL INFORMATION:
APPLICANT: BECKER et al.
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 108
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..(108)
OTHER INFORMATION: amino acid 'Xaa' can be any amino acid
US-09-147-875A-26

Query Match 83.9%; Score 439; DB 4; Length 108;
Best Local Similarity 88.0%; Pred. No. 6.3e-32;
Matches 95; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
Db 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNVXELEELSPPEIDLK 60
Qy 60 DAETNVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNHVEDYIKEGLEEAIAIKQAELKTPKELDAALNELGPDGDEEE 108

Search completed: November 17, 2005, 19:32:21
Job time : 21.5334 secs

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Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
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Db 1 LEDAELEKVLATLDPEGKTODELDKEAAAEALNKKVEALQNVQVAELEEELSLEDNLIK 60
QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 11
US-09-147-875A-25
; Sequence 25, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-25

Query Match 87.0%; Score 455; DB 4; Length 108;
Best Local Similarity 89.8%; Pred. No. 2.4e-33;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
QY 1 LEKAAELENLLSTLDPEGKTODELDKEAAAEALNKKVEALPNÖV-ELEEELSLEDNLIK 59
Db 1 LEDAELEKVLATLDPEGKTODELDKEAAAEALNKKVEALQNVQVAELEEELSLEDNLIK 60
QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 12
US-08-529-055-70
; Sequence 70, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-70

Query Match 87.0%; Score 455; DB 4; Length 232;
Best Local Similarity 89.8%; Pred. No. 6e-33;
Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
QY 1 LEKAAELENLLSTLDPEGKTODELDKEAAAEALNKKVEALPNÖV-ELEEELSLEDNLIK 59
Db 51 LEDAELEKVLATLDPEGKTODELDKEAAAEALNKKVEALQNVQVAELEEELSLEDNLIK 110
QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 111 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 158

RESULT 13
US-08-529-055-73
; Sequence 73, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-23

Query Match 92.0%; Score 481; DB 2; Length 108;
Best Local Similarity 95.4%; Pred. No. 1.2e-35;
Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 1 LEKAELENLLSTLDPGKTKQDELKKEAAEALNKKVEALPNQV-ELEBELSKLEDNLK 59
Db 1 LEKAGAGLGNLLSTLDPGKTKQDELKKEAAEALNKKVEALPNQVSELEBELSKLEDNLK 60

Qy 60 DAETN-VDYIKEGLEEAIAIKQAELEKTPKELDAALNELPGDGEDEE 106
Db 61 DAETNHVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELPGDGEDEE 108

RESULT 9
US-08-529-055-68
; Sequence 68, Application US/08529055
; Patent No. 6592876
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: Pneumococcal Genes, Portions
; TITLE OF INVENTION: Thereof, Expression Products
; TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
; TITLE OF INVENTION: Portions and Products
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,055
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-24

Query Match 87.0%; Score 455; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 2.4e-33;

; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-529-055-68

Query Match 92.0%; Score 481; DB 4; Length 212;
Best Local Similarity 95.4%; Pred. No. 2.7e-35;
Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 1 LEKAELENLLSTLDPGKTKQDELKKEAAEALNKKVEALPNQV-ELEBELSKLEDNLK 59
Db 28 LEKAGAGLGNLLSTLDPGKTKQDELKKEAAEALNKKVEALPNQVAELEBELSKLEDNLK 87

Qy 60 DAETN-VDYIKEGLEEAIAIKQAELEKTPKELDAALNELPGDGEDEE 106
Db 88 DAETNHVEDYIKEGLEEAIAIKQAELEKTPKELDAALNELPGDGEDEE 135

RESULT 10
US-08-710-749-24
; Sequence 24, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: n/a
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-710-749-24

Query Match 87.0%; Score 455; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 2.4e-33;
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ADDRESSEE: Curtis, Morris & Safford, P.C.
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/714,741
 FILING DATE: 16-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer Esq., William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454312-2460
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8991 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: amino acid
 US-08-714-741-32

Query Match 96.0%; Score 502; DB 4; Length 8991;
 Best Local Similarity 98.1%; Pred. No. 3.3e-35;
 Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 QY 1 LEKAEAELENLSTLDPEGKTQDELKAEAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 DB 7981 LEKAEAELENLSTLDPEGKTQDELKAEAEALNKKVEALPNQVSELEEELSKLEDNLK 8040
 QY 60 DAETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 DB 8041 DAETNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 8088

RESULT 6
 US-09-147-875A-24
 Sequence 24, Application US/09147875A
 Patent No. 6638516
 GENERAL INFORMATION:
 APPLICANT: BECKER et al.
 TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
 FILE REFERENCE: 454312-2471
 CURRENT APPLICATION NUMBER: US/09/147,875A
 CURRENT FILING DATE: 1999-05-24
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 24
 LENGTH: 108
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae
 US-09-147-875A-24

Query Match 93.3%; Score 488; DB 4; Length 108;
 Best Local Similarity 96.3%; Pred. No. 2.9e-36;
 Matches 104; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 LEKAEAELENLSTLDPEGKTQDELKAEAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 DB 1 LEKAGAGLNLSTLDPEGKTQDELKAEAEALNKKVEALPNQVAEELEEELSKLEDNLK 60
 QY 60 DAETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 DB 61 DAETNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 7
 US-08-710-749-22
 Sequence 22, Application US/08710749
 Patent No. 5955089
 GENERAL INFORMATION:
 APPLICANT: Briles, David E.
 APPLICANT: Hollingshead, Susan
 APPLICANT: Becker, Robert
 TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/710,749
 FILING DATE: 20-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454312-2074
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 STRANDEDNESS: n/a
 TOPOLOGY: linear
 MOLECULE TYPE: amino acid
 US-08-710-749-22

Query Match 92.0%; Score 481; DB 2; Length 108;
 Best Local Similarity 95.4%; Pred. No. 1.2e-35;
 Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 1 LEKAEAELENLSTLDPEGKTQDELKAEAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 DB 1 LEKAGAGLNLSTLDPEGKTQDELKAEAEALNKKVEALPNQVSELEEELSKLEDNLK 60
 QY 60 DAETN-VEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
 DB 61 DAETNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 8
 US-08-710-749-23
 Sequence 23, Application US/08710749
 Patent No. 5955089
 GENERAL INFORMATION:
 APPLICANT: Briles, David E.
 APPLICANT: Hollingshead, Susan
 APPLICANT: Becker, Robert
 TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 STREET: 530 Fifth Avenue
 CITY: New York

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,749
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-26

Query Match 96.0%; Score 502; DB 2; Length 108;
Best Local Similarity 98.1%; Pred. No. 1.7e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOV-ELEBELSKLEDNLK 59
Db 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOVSELEBELSKLEDNLK 60
Qy 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 3
US-09-147-875A-23
Sequence 23, Application US/09147875A
Patent No. 6638516
GENERAL INFORMATION:
APPLICANT: BECKER et al.
TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
FILE REFERENCE: 454312-2471
CURRENT APPLICATION NUMBER: US/09/147,875A
CURRENT FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 108
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-147-875A-23

Query Match 96.0%; Score 502; DB 4; Length 108;
Best Local Similarity 98.1%; Pred. No. 1.7e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOV-ELEBELSKLEDNLK 59
Db 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOVSELEBELSKLEDNLK 60
Qy 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 108

RESULT 4
US-08-529-055-67
Sequence 67, Application US/08529055
Patent No. 6592876
GENERAL INFORMATION:

APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-67

Query Match 96.0%; Score 502; DB 4; Length 211;
Best Local Similarity 98.1%; Pred. No. 3.7e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 1 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOV-ELEBELSKLEDNLK 59
Db 25 LEKAAELENLLSTLDPEGKTQDELKAAAEALNKKVEALPNOVSELEBELSKLEDNLK 84
Qy 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 106
Db 85 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEEE 132

RESULT 5
US-08-714-741-32
Sequence 32, Application US/08714741
Patent No. 6500613
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 18:59:20 ; Search time 20.4084 Seconds
(without alignments)
387.723 Million cell updates/sec

Title: US-10-674-755-22
Perfect score: 523
Sequence: 1 LEKAAELENLLSTLDPEGK.....TPKELDAALNELGPDGDEE 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 523 | 100.0 | 106 | 4 | US-09-147-875A-22 |
| 2 | 502 | 96.0 | 108 | 2 | US-08-710-749-26 |
| 3 | 502 | 96.0 | 108 | 4 | US-09-147-875A-23 |
| 4 | 502 | 96.0 | 211 | 4 | US-08-529-055-67 |
| 5 | 502 | 96.0 | 8991 | 4 | US-08-714-741-32 |
| 6 | 488 | 93.3 | 108 | 4 | US-09-147-875A-24 |
| 7 | 481 | 92.0 | 108 | 2 | US-08-710-749-22 |
| 8 | 481 | 92.0 | 108 | 2 | US-08-710-749-23 |
| 9 | 481 | 92.0 | 212 | 4 | US-08-529-055-68 |
| 10 | 455 | 87.0 | 108 | 2 | US-08-710-749-24 |
| 11 | 455 | 87.0 | 108 | 4 | US-09-147-875A-25 |
| 12 | 455 | 87.0 | 232 | 4 | US-08-529-055-70 |
| 13 | 455 | 87.0 | 458 | 4 | US-08-529-055-73 |
| 14 | 439 | 83.9 | 108 | 2 | US-08-710-749-25 |
| 15 | 439 | 83.9 | 108 | 4 | US-09-147-875A-26 |
| 16 | 413 | 79.0 | 185 | 4 | US-08-529-055-69 |
| 17 | 319 | 61.0 | 104 | 2 | US-08-710-749-20 |
| 18 | 315 | 60.2 | 213 | 4 | US-08-529-055-47 |
| 19 | 311 | 59.5 | 104 | 4 | US-09-147-875A-21 |
| 20 | 309 | 59.1 | 104 | 2 | US-08-710-749-19 |
| 21 | 309 | 59.1 | 104 | 4 | US-09-147-875A-20 |
| 22 | 303 | 57.9 | 641 | 3 | US-08-961-083-160 |
| 23 | 303 | 57.9 | 641 | 4 | US-09-536-784-160 |
| 24 | 300 | 57.4 | 197 | 4 | US-08-529-055-44 |
| 25 | 288 | 55.1 | 102 | 2 | US-08-710-749-21 |
| 26 | 288 | 55.1 | 102 | 4 | US-09-147-875A-18 |
| 27 | 275 | 52.6 | 233 | 4 | US-08-529-055-52 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 257.5 | 49.2 | 119 | 2 | US-08-710-749-27 | Sequence 27, Appl |
| 29 | 257.5 | 49.2 | 119 | 4 | US-09-147-875A-27 | Sequence 27, Appl |
| 30 | 257.5 | 49.2 | 215 | 4 | US-08-529-055-43 | Sequence 43, Appl |
| 31 | 225 | 43.0 | 80 | 2 | US-08-710-749-18 | Sequence 18, Appl |
| 32 | 225 | 43.0 | 80 | 4 | US-09-147-875A-19 | Sequence 19, Appl |
| 33 | 194 | 37.1 | 288 | 3 | US-08-312-949-4 | Sequence 4, Appl |
| 34 | 194 | 37.1 | 288 | 3 | US-08-446-201-4 | Sequence 4, Appl |
| 35 | 194 | 37.1 | 619 | 1 | US-08-465-746-2 | Sequence 2, Appl |
| 36 | 194 | 37.1 | 619 | 1 | US-08-214-164-2 | Sequence 2, Appl |
| 37 | 194 | 37.1 | 619 | 2 | US-08-467-852A-3 | Sequence 3, Appl |
| 38 | 194 | 37.1 | 619 | 2 | US-08-246-636-2 | Sequence 2, Appl |
| 39 | 194 | 37.1 | 619 | 2 | US-08-247-491A-3 | Sequence 3, Appl |
| 40 | 194 | 37.1 | 619 | 2 | US-08-319-795-2 | Sequence 2, Appl |
| 41 | 194 | 37.1 | 619 | 2 | US-08-468-985-2 | Sequence 2, Appl |
| 42 | 194 | 37.1 | 619 | 3 | US-08-312-949-2 | Sequence 2, Appl |
| 43 | 194 | 37.1 | 648 | 1 | US-08-072-070-2 | Sequence 2, Appl |
| 44 | 194 | 37.1 | 648 | 1 | US-08-469-434-2 | Sequence 2, Appl |
| 45 | 194 | 37.1 | 648 | 1 | US-08-214-222-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-09-147-875A-22
; Sequence 22, Application US/09147875A
; Patent No. 6638516
; GENERAL INFORMATION:
; APPLICANT: BECKER et al.
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE PROTEINS
; FILE REFERENCE: 454312-2471
; CURRENT APPLICATION NUMBER: US/09/147,875A
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 22
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-147-875A-22

Query Match 100.0%; Score 523; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.3e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEKAAELENLLSTLDPEGKTODELDKEAAEALNKKVEALPNQVELEEELSKLEDNLKD 60
DB 1 LEKAAELENLLSTLDPEGKTODELDKEAAEALNKKVEALPNQVELEEELSKLEDNLKD 60
QY 61 AETNVEDYIKGLEAEATKQAELEKTPKELDAALNELGPDGDEEE 106
DB 61 AETNVEDYIKGLEAEATKQAELEKTPKELDAALNELGPDGDEEE 106

RESULT 2
US-08-710-749-26
; Sequence 26, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=20;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF255548; AAF68101.1; -.
DR HSSP; P04268; IIC2.
FT NON_TER 1
FT NON_TER 231
SQ SEQUENCE 231 AA; 24990 MW; A7731E3A46460186 CRC64;

Query Match      58.5%; Score 306; DB 2; Length 231;
Best Local Similarity 63.6%; Fred. No. 1.3e-10;
Matches 68; Conservative 12; Mismatches 23; Indels 4; Gaps 2;

Qy 1 LEKAAELENLLSTLDPEGKTQDELDEKAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
   | : ||||| ||||| ||||| ||||| ||||| : || : || : || : || : ||
Db 76 LAKKQTELEKLLDNLDPGKTQDELDEKAAEALNKKVEALPNQV-ELEEELSKLEDNLK 135

Qy 60 DAETNVEDYIKEGLEEAIAIKOAELEKTPKELDAALNELGPDGDEE 106
   | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 GADPEDD---TAALQNKLATKKAELEKTKQKELDAALNELGPDGDEE 179

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Search completed: November 17, 2005, 20:37:52
 Job time : 63.8331 secs

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Qy 105 EE 106
Db 140 EE 141

RESULT 14
Q9J584 PRELIMINARY; PRT; 222 AA.
ID Q9L584
AC Q9L584;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=43;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP255543; AAF68096.1; -.
DR HSP; P04268; IIC2.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 23952 MW; 4824321A80C658B0 CRC64;

Query Match 58.9%; Score 308; DB 2; Length 222;
Best Local Similarity 64.5%; Pred No. 9.4e-11;
Matches 69; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

Qy 1 LEKAAEALENLLSTLDPEGKTQDELKQAEALNKVQV-ELEBELSKLEDNLK 59
Db 32 LAKQTGLEKLDLSDPEGKTQDELKQAEALNKVQVADLEKEISNLEILG 91

Qy 60 DARTNVEDYIKGLEEAIAATQKALEKTPKELDAALNELPGDGEDE 106
Db 92 GADPEDD---TAALQNKLATTKALEKTKQELDAALNELPGDGEDE 135

RESULT 15
Q9J579 PRELIMINARY; PRT; 231 AA.
ID Q9L579
AC Q9L579;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=20;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).

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ID Q8GNT0 PRELIMINARY; PRT; 211 AA.
AC Q8GNT0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP95;
RX MEDLINE=22241996; PubMed=12354862;
RA Diuonzo G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Pantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
RT Italian patients.";
RL J. Clin. Microbiol. 40:3660-3665(2002).
DR EMBL; AF490265; AAN37733.1; -.
FT NON_TER 1
FT NON_TER 211
SQ SEQUENCE 211 AA; 23207 MW; 096BPFBE08CD6483 CRC64;

Query Match 65.5%; Score 342.5; DB 2; Length 211;
Best Local Similarity 64.7%; Pred. No. 8.8e-13;
Matches 77; Conservative 12; Mismatches 17; Indels 13; Gaps 4;

Qy 1 LEKAEAELENLSTLDPEGKTQDELDEKAAE-----AEINKKVEALPNQV-ELEBELSKLE 55
Db 5 LEKAEAELENLSTLDPEGKTQDELDEKAAEDVNEALQNKVADLENKVAELDKVETRLQ 64

Qy 56 DNLKDA-ETNVEDYIKEGLEAIAIKQAELEKT-----PKELDAALNELGPDGDEE 106
Db 65 SLDKDAEENNVEDYIKEGLEKALTDTKKVELNNTQKALDTAPKALDTALNELGPDGDEE 123

RESULT 10
ID Q9LAX6 PRELIMINARY; PRT; 461 AA.
AC Q9LAX6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC6303;
RX MEDLINE=20448953; PubMed=10992499;
RX DOI=10.1128/IAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RT in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071820; AAF27715.1; -.
FT NON_TER 461
FT NON_TER 461
SQ SEQUENCE 461 AA; 51563 MW; 249435F6558B92 CRC64;

Query Match 62.8%; Score 328.5; DB 2; Length 461;
Best Local Similarity 59.0%; Pred. No. 1.2e-11;
Matches 72; Conservative 16; Mismatches 15; Indels 19; Gaps 4;

Qy 1 LEKAEAELENLSTLDPEGKTQDELDEKAAEAEALNKVKVEALPNQV-----ELEBELS 52
Db 273 LEDAELEKVLATLDPEGKTQDELDEKAAE---DANIEALQNKVADLENKVAELDKVET 329

Qy 53 KLEDNLKDA-ETNVEDYIKEGLEAIAIKQAELEKT-----PKELDAALNELGPDGDEE 104
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Db 330 RLQSDLKDAEENNVEDYIKEGLEKALTDTKKVELNNTQKALDTAPKALDTALNELGPDGDE 389
Qy 105 EE 106
Db 390 EE 391

RESULT 11
ID Q9L562 PRELIMINARY; PRT; 242 AA.
AC Q9L562;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=69;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=69;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF255308; AAF70098.1; -.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 25843 MW; 707EA930797D2C82 CRC64;

Query Match 61.4%; Score 321; DB 2; Length 242;
Best Local Similarity 66.4%; Pred. No. 1.8e-11;
Matches 71; Conservative 13; Mismatches 19; Indels 4; Gaps 2;

Qy 1 LEKAEAELENLSTLDPEGKTQDELDEKAAEAEALNKVKVEALPNQV-ELEBELSKLEDNLK 59
Db 70 LAKQTELEKLDLSDPEGKTQDELDEKAAEAEALDKKVAELQNKVADLEKESINLEILG 129

Qy 60 DAEINVEDYIKEGLEAIAIKQAELEKT-----PKELDAALNELGPDGDEE 106
Db 130 GADSEDD---TAALQNKLATKAALEKTQKELDAALNELGPDGDEE 173

RESULT 12
ID Q9L595 PRELIMINARY; PRT; 256 AA.
AC Q9L595;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP220;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
```

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKELDNLK 59
|||||
Db 295 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALQNQVAEEELSKELDNLK 354
|||||
QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 106
|||||
Db 355 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKQDVAALNDLVPDGGEE 402
|||||

RESULT 6

Q8GNS7 ID Q8GNS7 PRELIMINARY; PRT; 213 AA.
AC Q8GNS7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=128;
RX MEDLINE=22241996; PubMed=12354862;
RA Dicunzio G., Gherardi G., Gertz R.E., D'Ambrosio F., Goglio A.,
RA Lorino G., Recchia S., Fantosti A., Beall B.;
RT "Genotypes of invasive pneumococcal isolates recently recovered from
Italian patients."
RL J. Clin. Microbiol. 40:3660-3665(2002).
RL EMBL; AF490268; AAN37736.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 23490 MW; 2384428409526EAB CRC64;

Query Match 87.0%; Score 455; DB 2; Length 213;

Best Local Similarity 90.7%; Pred. No. 2.6e-19;

Matches 98; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKELDNLK 59
|||||
Db 26 LEKAAELENLLSTLDPEGKTQDELDKETAEEALNKKVEALQNQVAEEELSKELDNLK 85
|||||

QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 106
|||||

Db 86 VAETNNVEDYIKEGLEEAIAATKQAELEKTPKALDTALNELGPDGDEE 133
|||||

RESULT 7

Q34097 ID Q34097 PRELIMINARY; PRT; 653 AA.
AC Q34097;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PspA.
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF5668;
RX MEDLINE=98427139; PubMed=9746574;
RA McDaniel L.S., McDaniel D.O., Hollingshead S.K., Briles D.E.;
RT "Comparison of the PspA sequence from Streptococcus pneumoniae EF5668
to the previously identified PspA sequence from strain Rxl and ability
of PspA from EF5668 to elicit protection against pneumococci of
different capsular types."
RL Infect. Immun. 66:4748-4754(1998).

DR EMBL; U89711; AAC62252.1; -.

DR HSSP; P06653; LHCK.

DR InterPro; IPR002479; CW binding.

DR InterPro; IPR002345; Lipocalin.

DR InterPro; IPR009053; Prefoldin.

DR Pfam; PF01473; CW binding_1; 9.

DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.

SQ SEQUENCE 653 AA; 73058 MW; CF147A96125120FA CRC64;

Query Match 87.0%; Score 455; DB 2; Length 653;

Best Local Similarity 89.8%; Pred. No. 7.8e-19;

Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKELDNLK 59
|||||

Db 276 LEDAELEKVLATLDPEGKTQDELDKAAAEALNKKVEALQNQVAEEELSKELDNLK 335
|||||

QY 60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 106
|||||

Db 336 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 383
|||||

RESULT 8

Q9L594 ID Q9L594 PRELIMINARY; PRT; 257 AA.
AC Q9L594;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RX MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
pneumococcal strains in the United States and of internationally
disseminated clones."
RL J. Clin. Microbiol. 38:3663-3669(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP222;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF254255; AAF68090.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 257 257
SQ SEQUENCE 257 AA; 28241 MW; 8470B68C949A133D CRC64;

Query Match 65.7%; Score 343.5; DB 2; Length 257;

Best Local Similarity 62.3%; Pred. No. 9.4e-13;

Matches 76; Conservative 14; Mismatches 13; Indels 19; Gaps 4;

QY 1 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELS 52
|||||

Db 51 LEKAAELENLLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKEVT 107
|||||

QY 53 KLEDNLKDA-ETNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDE 104
|||||

Db 108 RQSDLKDAEENNVEDYIKEGLEKALTDKKVELNNTQALDTALNELGPDGDE 167
|||||

QY 105 EE 106
||

Db 168 EE 169
||

RESULT 9

Q8GNT0

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=BG11703;
RX  MEDLINE=20448953; PubMed=10992499;
RY  DOI=10.1128/JAI.68.10.5889-5900.2000;
RA  Hollingshead S.K., Becker R., Briles D.E.;
RT  "Diversity of PspA: mosaic genes and evidence for past recombination
RL  in Streptococcus pneumoniae.";
DR  EMBL; AF071821; AAF27716.1; -.
DR  HSSP; P58301; 1L8D.
FT  NON TER 481
SQ  SEQUENCE 481 AA; 53500 MW; EA3C66445EFCE2B CRC64;

Query Match 92.9%; Score 486; DB 2; Length 481;
Best Local Similarity 96.3%; Pred. No. 9.1e-21;
Matches 104; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY  1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
DB  |||||
DB  295 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALQNVQVAEELEELSKLEDNLK 354
QY  60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 106
DB  |||||
DB  355 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 402

RESULT 3
Q9L5B4 PRELIMINARY; PRT; 246 AA.
AC Q9L5B4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SP198;
RY MEDLINE=20472698; PubMed=11015380;
RA Beall B., Gherardi G., Facklam R.R., Hollingshead S.K.;
RT "Pneumococcal pspA sequence types of prevalent multiresistant
RT pneumococcal strains in the United States and of internationally
RT disseminated clones.";
RL J. Clin. Microbiol. 38:3663-3669(2000).
[2]
RP SEQUENCE FROM N.A.
RX STRAIN=SP198;
RY MEDLINE=20472698; PubMed=11015380;
RA Beall B.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253408; AAF67356.1; -.
DR HSSP; P05412; 1JNM.
FT NON TER 1
FT NON TER 246
SQ SEQUENCE 246 AA; 26972 MW; 2190EED1460D26D9 CRC64;

Query Match 92.2%; Score 482; DB 2; Length 246;
Best Local Similarity 95.4%; Pred. No. 8.1e-21;
Matches 103; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY  1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
DB  |||||
DB  52 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALQNVQVAEELEELSKLEDNLK 111
QY  60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 106
DB  |||||
DB  112 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 159

us-10-674-755-22.rup

RESULT 4
Q8KQK2 PRELIMINARY; PRT; 107 AA.
AC Q8KQK2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Pneumococcal surface protein A (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=255/00;
RY MEDLINE=22170754; PubMed=12183557;
RY DOI=10.1128/JAI.70.9.5086-5090.2002;
RA Miyaji E.N., Ferreira D.M., Lopes A.P.V., Brandileone M.C.C.,
RA Dias W.O., Leite L.C.C.;
RT "Analysis of serum cross-reactivity and cross-protection elicited by
RT immunization with DNA vaccines against Streptococcus pneumoniae
RT expressing PspA fragments from different clades.";
RL Infect. Immun. 70:5086-5090(2002).
DR EMBL; AY082390; AAL92495.1; -.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11897 MW; 47913E25EE47D5CC CRC64;

Query Match 91.2%; Score 477; DB 2; Length 107;
Best Local Similarity 95.3%; Pred. No. 7e-21;
Matches 102; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY  1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
DB  |||||
DB  1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALQNVQVAEELEELSKLEDNLK 60
QY  60 DAET-NVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 105
DB  |||||
DB  61 DAETNNVEDYIKEGLEEAIAATKQAELEKTPKELDAALNELGPDGDEE 107

RESULT 5
Q9LAX3 PRELIMINARY; PRT; 480 AA.
AC Q9LAX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PspA (Fragment).
GN Name=pspA;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BG7561;
RY MEDLINE=20448953; PubMed=10992499;
RY DOI=10.1128/JAI.68.10.5889-5900.2000;
RA Hollingshead S.K., Becker R., Briles D.E.;
RT "Diversity of PspA: mosaic genes and evidence for past recombination
RL in Streptococcus pneumoniae.";
RL Infect. Immun. 68:5889-5900(2000).
DR EMBL; AF071824; AAF27718.1; -.
DR InterPro; IPR000533; Tropomyosin.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON TER 480
FT NON TER 480
SQ SEQUENCE 480 AA; 53043 MW; DA013C9E0190D7A0 CRC64;

Query Match 88.1%; Score 461; DB 2; Length 480;
Best Local Similarity 91.7%; Pred. No. 2.6e-19;
Matches 99; Conservative 3; Mismatches 4; Indels 2; Gaps 2;

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OM protein - protein search, using sw model

Run On: November 17, 2005, 19:32:37 ; Search time 62.8331 Seconds
(without alignments)
863.882 Million cell updates/sec

Title: US-10-674-755-22
Perfect score: 523
Sequence: 1 LEKAEAELENLSTLDPEGK.....TPKELDAALNELGPDGDEEE 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 486 | 92.9 | 479 | Q9LAX2 | Q9lax2 streptococc |
| 2 | 486 | 92.9 | 481 | Q9LAX5 | Q9lax5 streptococc |
| 3 | 482 | 92.2 | 246 | Q9L5B4 | Q9l5b4 streptococc |
| 4 | 477 | 91.2 | 107 | Q8KOK2 | Q8kgk2 streptococc |
| 5 | 461 | 88.1 | 480 | Q9LAX3 | Q9lax3 streptococc |
| 6 | 455 | 87.0 | 213 | Q8GNS7 | Q8gns7 streptococc |
| 7 | 455 | 87.0 | 653 | Q34097 | Q34097 streptococc |
| 8 | 343.5 | 65.7 | 257 | Q9L594 | Q9l594 streptococc |
| 9 | 342.5 | 65.5 | 211 | Q8GNT0 | Q8gnt0 streptococc |
| 10 | 328.5 | 62.8 | 461 | Q9LAX6 | Q9lax6 streptococc |
| 11 | 321 | 61.4 | 242 | Q9L562 | Q9l562 streptococc |
| 12 | 320.5 | 61.3 | 256 | Q9L595 | Q9l595 streptococc |
| 13 | 317.5 | 60.7 | 227 | Q9KGS0 | Q9kgs0 streptococc |
| 14 | 308 | 58.9 | 222 | Q9L584 | Q9l584 streptococc |
| 15 | 306 | 58.5 | 231 | Q9L579 | Q9l579 streptococc |
| 16 | 306 | 58.5 | 241 | Q9L580 | Q9l580 streptococc |
| 17 | 304 | 58.1 | 228 | Q9L588 | Q9l588 streptococc |
| 18 | 304 | 58.1 | 235 | Q9L582 | Q9l582 streptococc |
| 19 | 304 | 58.1 | 249 | Q9L5D4 | Q9l5d4 streptococc |
| 20 | 304 | 58.1 | 252 | Q9L583 | Q9l583 streptococc |
| 21 | 304 | 58.1 | 360 | Q8KOK3 | Q8kgk3 streptococc |
| 22 | 304 | 58.1 | 429 | Q9LAX7 | Q9lax7 streptococc |
| 23 | 304 | 58.1 | 526 | Q9LAX9 | Q9lax9 streptococc |
| 24 | 304 | 58.1 | 608 | Q8VQ55 | Q8vq55 streptococc |
| 25 | 304 | 58.1 | 744 | Q97T39 | Q97t39 streptococc |
| 26 | 302 | 57.7 | 249 | Q9L5B7 | Q9l5b7 streptococc |
| 27 | 302 | 57.7 | 502 | Q9LAX8 | Q9lax8 streptococc |
| 28 | 301 | 57.6 | 249 | Q9L585 | Q9l585 streptococc |
| 29 | 301 | 57.6 | 256 | Q9L590 | Q9l590 streptococc |
| 30 | 294 | 56.2 | 209 | Q9L593 | Q9l593 streptococc |
| 31 | 202 | 38.6 | 417 | Q9LAY3 | Q9lay3 streptococc |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 32 | 194 | 37.1 | 619 | 2 | Q54972 | Q54972 streptococc |
| 33 | 194 | 37.1 | 619 | 2 | Q8DR10 | Q8dri0 streptococc |
| 34 | 183 | 35.0 | 415 | 2 | Q9LAY1 | Q9lay1 streptococc |
| 35 | 167 | 31.9 | 739 | 2 | Q9ROT4 | Q9rot4 streptococc |
| 36 | 167 | 31.9 | 820 | 2 | Q9ROT1 | Q9rot1 streptococc |
| 37 | 167 | 31.9 | 929 | 2 | Q9KK19 | Q9kk19 streptococc |
| 38 | 167 | 31.9 | 929 | 2 | Q9ZAY5 | Q9zay5 streptococc |
| 39 | 165 | 31.5 | 249 | 2 | Q9L575 | Q9l575 streptococc |
| 40 | 158 | 30.2 | 426 | 2 | Q9LAY5 | Q9lay5 streptococc |
| 41 | 157 | 30.0 | 224 | 2 | Q8GNS8 | Q8gns8 streptococc |
| 42 | 152.5 | 29.2 | 869 | 2 | Q9KK27 | Q9kk27 streptococc |
| 43 | 152 | 29.1 | 99 | 2 | Q8KQK4 | Q8kqk4 streptococc |
| 44 | 151 | 28.9 | 395 | 2 | Q9LAY2 | Q9lay2 streptococc |
| 45 | 151 | 28.9 | 408 | 2 | Q9LAY0 | Q9lay0 streptococc |

ALIGNMENTS

RESULT 1

| | | | | | |
|--------|--|--------------|------|-----|-----|
| Q9LAX2 | | | | | |
| ID | Q9LAX2 | PRELIMINARY; | PRT; | 479 | AA. |
| AC | Q9LAX2; | | | | |
| DT | 01-OCT-2000 (Tremblrel. 15, Created) | | | | |
| DT | 01-OCT-2000 (Tremblrel. 15, Last sequence update) | | | | |
| DE | PspA (Fragment). | | | | |
| GN | Name=PspA; | | | | |
| OS | Streptococcus pneumoniae. | | | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | | |
| OC | Streptococcus. | | | | |
| OX | NCBI_TaxID=1313; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=BG7817; | | | | |
| RX | MEDLINE=20448953; PubMed=10992499; | | | | |
| RX | DOI=10.1128/IAI.68.10.5889-5900.2000; | | | | |
| RA | Hollingshead S.K., Becker R., Briles D.E.; | | | | |
| RT | "Diversity of PspA: mosaic genes and evidence for past recombination in Streptococcus pneumoniae"; | | | | |
| RL | Infect. Immun. 68:5889-5900(2000). | | | | |
| DR | EMBL; AF071826; AAF7719.1; - | | | | |
| DR | InterPro; IPR000533; Tropomyosin. | | | | |
| FT | PRINTS; PR00194; TROPOMYOSIN. | | | | |
| FT | NON_TER 479 479 | | | | |
| SQ | SEQUENCE 479 AA; 53257 MW; B9C0D2CA15DE3654 CRC64; | | | | |

Query Match 92.9%; Score 486; DB 2; Length 479;
Best Local Similarity 96.3%; Pred. No. 9.1e-21;
Matches 104; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

| | | |
|----|-----|--|
| Qy | 1 | LEKAEAELENLSTLDPEGKTQDELDEKAEAELENKKVEALPNQV-ELEBELSKLEDNLK 59 |
| Dd | 295 | LEKAEAELENLSTLDPEGKTQDELDEKAEAELENKKVEALQNVAELEBELSKLEDNLK 354 |
| Qy | 60 | DAET-NVEDYIKESLEBAIATKQAELEKTPKELDAALNELGPDGDEEE 106 |
| Dd | 355 | DAETNNVEDYIKESLEBAIATKQAELEKTPKELDAALNELGPDGDEEE 402 |

RESULT 2

| | | | | | |
|--------|--|--------------|------|-----|-----|
| Q9LAX5 | | | | | |
| ID | Q9LAX5 | PRELIMINARY; | PRT; | 481 | AA. |
| AC | Q9LAX5; | | | | |
| DT | 01-OCT-2000 (Tremblrel. 15, Created) | | | | |
| DT | 01-OCT-2000 (Tremblrel. 15, Last sequence update) | | | | |
| DE | PspA (Fragment). | | | | |
| GN | Name=PspA; | | | | |
| OS | Streptococcus pneumoniae. | | | | |
| OC | Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; | | | | |
| OC | Streptococcus. | | | | |
| OX | NCBI_TaxID=1313; | | | | |

QY 89 KELDAAALNE 97
 Db 1096 SEVKAOLKE 1104

RESULT 13

A61231
 myosin heavy chain nonmuscle form A - human
 N:Alternate names: cellular myosin heavy chain; myosin type 9; NMHC-A
 N:Contains: myosin ATPase (EC 3.6.4.1)
 C:Species: Homo sapiens (man)
 C:Date: 12-May-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
 C:Accession: A61231; A34876; I52562; I61692
 R:Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, C.
 Circ. Res. 69, 530-539, 1991
 A:Title: Human nonmuscle myosin heavy chains are encoded by two genes located on different chromosomes
 A:Reference number: A61231; MUID:91316803; PMID:1860190
 A:Accession: A61231
 A:Molecule type: mRNA
 A:Residues: 1-715 <SIM>
 A:Cross-references: UNIPROT:P35579; UNIPROT:Q9UMJ0; GB:M69180; NID:g189029; PIDN:AAA61768
 R:Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990
 A:Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alternative splicing
 A:Reference number: A34876; MUID:90138958; PMID:1967836
 A:Accession: A34876
 A:Molecule type: mRNA
 A:Residues: 715-1961 <SAB>
 A:Cross-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036
 R:Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.; Blood 78, 1826-1833, 1991
 A:Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, cDNA sequencing, and expression in transgenic mice
 A:Reference number: I52562; MUID:92003925; PMID:1912569
 A:Accession: I52562
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-52, 'EAY', 56-659, 'T', 661-868, 'T', 870-930, 'C', 932-1239, 'KG', 1242-1337 <RES>
 A:Cross-references: GB:M81105; NID:g188988; PIDN:AAAS9888.1; PID:g553596
 R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
 A:Title: Identification and overlapping expression of multiple unconventional myosin genes in Dictyostelium
 A:Reference number: A55758; MUID:94294418; PMID:8022818
 A:Accession: I61692
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 182-218 <BEM>
 A:Cross-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134
 C:Genetics:
 A:Gene: GDB:MYH9
 A:Cross-references: GDB:120216; OMIM:160775
 A:Map position: 22q12.3-22q13.1
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide binding site
 F:84-764/Domain: myosin motor domain homology <MMOT>
 F:174-181/Region: nucleotide-binding motif A (P-loop)
 F:552-565/Region: actin binding #status predicted
 F:626-640/Region: actin binding #status predicted
 F:837-1938/Domain: coiled coil #status predicted <COI>
 F:837-1277/Domain: S2 #status predicted <DS2>
 F:1278-1961/Domain: light meromyosin #status predicted <LMM>
 F:1939-1961/Domain: carboxyl-terminal <CBT>
 F:125/Modified site: N6,N6-trimethyllysine (lys) #status predicted
 F:180/Binding site: ATP (lys) #status predicted
 F:694,704/Active site: Cys #status predicted

Query Match 20.7%; Score 108; DB 1; Length 1961;
 Best Local Similarity 29.5%; Pred. No. 26;
 Matches 33; Conservative 26; Mismatches 35; Indels 18; Gaps 4;

QY 2 EKAE-----AELNLLSTLDPEKGTQDELDKAEAAELNKKVYALPNQV-ELEEL 51
 Db 1492 OKAELRINKOFRYEMEDLMSSKDDVKGSKVHELEK--SKRALEOOVEEMKTGLELEL 1549

[illegible]

| | | | | |
|----|------|--|---|----|
| QY | 2 | EKAE----- | ALENLLSTLDPEGKTQDELDKEAAEALNKKVEALPNQV-ELEBEL | 51 |
| DB | 1492 | OKAEERLNKQFRTMEDLMSSKDDVGRSVHELEK--SKRALEOOVEEMKTOLEEBEL | 1549 | |

myosin heavy chain form B, nonmuscle - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A47297; A55441
R;Bhatia-Dey, N.; Adelstein, R.S.; Dawid, I.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993
A/Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmuscle
A/Reference number: A47297; MUID:93219383; PMID:8464900
A/Accession: A47297
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1992 <BHA>
A/Cross-references: UNIPROT:Q04834; GB:L09740; NID:G214623; PIDN:AAAA49915.1; PID:G214624
A/Experimental source: XTC cells
A/Note: sequence extracted from NCBI backbone (NCBIP:128722)
R;Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.
J. Biol. Chem. 270, 1395-1401, 1995
A/Title: A Xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-B34 (C
A/Reference number: A55441; MUID:95138137; PMID:7836406
A/Accession: A55441
A/Status: preliminary
A/Molecule type: protein
A/Residues: 198-232 <KEL>
C/Superfamily: myosin heavy chain; myosin motor domain homology
C/Keywords: nucleotide binding; P-loop
F;88-787/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 20.8%; Score 109; DB 2; Length 1992;
Best Local Similarity 30.5%; Pred. No. 23;
Matches 32; Conservative 27; Mismatches 42; Indels 4; Gaps 3;

QY 2 EKAAELENLLSTLDPSGKTQDELDKAAEALNKKVEALPNQV-ELEBELSKLENLKD 60
DB 1522 KQRAEMEDLMSSKDDVGNKVHELEK--SKRALDQGVEMRTQLEBELOQTEDAKLR 1579
QY 61 AETNVEDYIKEGLEALATQAELEKTPKELDAALNELGPDGDEE 105
DB 1580 LEVNMQ-AMKAQFERDLQTRDQNEKKRALVKQVRELEAELEDE 1623

RESULT 12
F84730
probable myosin heavy chain [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: F84730
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; J
eaus, D.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: F84730
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1269 <STO>

```

A;CrossReferences: GB:AE002095; MID:G9336463; FALD:AMC09932.2; GSFDB:GN00133
C;Genetics:
A;Gene: At2g32240
A;Map position: 2

      Query Match      20.7%; Score 108; DB 2; Length 1269;
      Best Local Similarity 31.8%; Pred. No. 17;
      Matches 41; Conservative 23; Mismatches 33; Indels 32; Gaps 6;

Qy      1 LEKAAEAELENLSTLDPGKQTQDRLDKAAE-AELNKKEV-ALPNQ-----VELEEELSKL 54
      976 LEDALSKLNETLIELGAKCOGKEGSLAEVNLKLNLELNAHNGSEANELQTKLSAL 1035

Db

```

```

QY      55 E-----DNLKOAEATNVDYIKGLEE-----AIATKQA-----ELEKTP 88
          :   :   :   :   :   :   :   :   :   :   :   :   :   :
1036 EAQEKEQTANLEASKTITIEDTKLTGEKELQSIEKLRAVAABKSVLSEHFEELKTL 1095

```

A;Reference number: A59287; MUID:93211444; PMID:8459827
A;Accession: A59287
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1940 <WES>
A;Cross-references: UNIPROT:Q02456; GB:L01634; PIDN:AAA29905.1
A;Experimental source: strain Brazilian LE
C;Genetics:
C;Gene: MYH
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;82-752/Domain: myosin motor domain homology <MMO>

Query Match 21.6%; Score 113; DB 2; Length 1940;
Best Local Similarity 28.5%; Pred. No. 12;
Matches 47; Conservative 22; Mismatches 36; Indels 60; Gaps 8;

QY 1 LEKAAEAE---LENLSTLDPGKTQDEL-----DK-----EAAEAE-----L 34

```

Qy      35 NK---KVEALPNQVE-----LEELSLEDNLKDQETNVEDY--IKEGLEEAI 77
||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db     1007 NKKAKLESTLDEMEENLAREQIRGDVSKRKGDLGDKATQETVDLLERVVRDLEQL 1066

Qy      78 ATKQAE-----LEKTPKELDAALNELPGDGEE 105
||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db     1067 RRKEABIGGLSGKFEDQGLVAOLQRKIKELQTRIQLEEDLEAE 1111

RESULT 9
```

N; Alternate names: surface antigen, 200K
C; Species: Schistosoma mansoni
C; Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C; Accession: S33068
R; Soilsion, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M.
J. Immunol. 149, 3612-3620, 1992
A; Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment of
A; Reference number: A45514; MUID:93056536; PMID:1431131
A; Accession: S33068
A; Molecule type: mRNA
A; Residues: 1-527 <SOI>
A; Cross-references: UNIPROT:Q65589; EMBL:X65591
A; Note: the authors translated the codon CAA for residue 346 as Lys
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: ATP; surface antigen
Query Match 21.4%; Score 112; DB 2; Length 527;
Best Local Similarity 28.5%; Pred. No. 3.8;

[illegible]

RESULT 10
I38055
myosin heavy chain, perinatal skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence revision 17-May-1996 #text change 09-Jul-2004

N;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:AE007317; PIDN:AAK98925.1; PID:gl
C;Genetics:
A;Gene: pspA

Query Match 37.1%; Score 194; DB 2; Length 619;
Best Local Similarity 45.9%; Pred. No. 3.2e-05;
Matches 51; Conservative 17; Mismatches 23; Indels 20; Gaps 4;

Qy 6 AELENLLSTLDPGKTQDELQKE-----AAAEINLKKVEALPNQV-ELE 48
Db 210 AELENQVHRLQELKEIDSESDYAKGFRAPLQSKLDAAKXLS-KLEELSDKIDELD 268

Qy 49 EELSKLENLKDAB--TWVEDYIKGLEEAATQAELEKTPKELDAAINE 97
Db 269 AEIAKLEDLQKAAEENNNVEDYFKEGLEKTTAAKKAELKTEADLKXAVNE 319

RESULT 3

A41971
surface protein pspA precursor - Streptococcus pneumoniae
N;Alternate names: pneumococcal surface protein A
C;Species: Streptococcus pneumoniae
C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A41971; A60282; A33134
R;Other: J.; Briles, D.E.
J. Bacteriol. 174, 601-609, 1992
A;Title: Structural properties and evolutionary relationships of PspA, a surface protein
A;Reference number: A41971; MUID:92105030; PMID:1729249
A;Accession: A41971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-619 <YOT>
A;Cross-references: UNIPROT:Q54972; UNIPROT:Q8DRI0; GB:M74122; NID:G153840; PIDN:AAA2701
A;Note: sequence extracted from NCBI backbone (NCBI:75635, NCBI:75636)
R;Talkington, D.F.; Crimmins, D.L.; Voellinger, D.C.; Yother, J.; Briles, D.E.
Infect. Immun. 59, 1285-1289, 1991
A;Title: A 43-kilodalton pneumococcal surface protein, PspA: isolation, protective ability
A;Reference number: A60282; MUID:91169598; PMID:2004810
A;Accession: A60282
A;Molecule type: protein
A;Residues: 32-76 <TAL>
A;Experimental source: strain JY2008
C;Genetics:
A;Gene: pspA
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-619/Product: surface protein pspA #status predicted <MAT>
F;411-430/Domain: cpl repeat homology <CP01>
F;431-450/Domain: cpl repeat homology <CP02>
F;451-470/Domain: cpl repeat homology <CP03>
F;471-490/Domain: cpl repeat homology <CP04>
F;491-510/Domain: cpl repeat homology <CP05>
F;511-530/Domain: cpl repeat homology <CP06>
F;531-550/Domain: cpl repeat homology <CP07>
F;551-570/Domain: cpl repeat homology <CP08>
F;571-591/Domain: cpl repeat homology <CP09>
F;592-611/Domain: cpl repeat homology <CP10>

Query Match 37.1%; Score 194; DB 2; Length 619;
Best Local Similarity 45.9%; Pred. No. 3.2e-05;
Matches 51; Conservative 17; Mismatches 23; Indels 20; Gaps 4;

Qy 6 AELENLLSTLDPGKTQDELQKE-----AAAEINLKKVEALPNQV-ELE 48
Db 210 AELENQVHRLQELKEIDSESDYAKGFRAPLQSKLDAAKXLS-KLEELSDKIDELD 268

Qy 49 EELSKLENLKDAB--TWVEDYIKGLEEAATQAELEKTPKELDAAINE 97
Db 269 AEIAKLEDLQKAAEENNNVEDYFKEGLEKTTAAKKAELKTEADLKXAVNE 319

RESULT 4

A40997
myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)

N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Aequipecten irradians
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A40997; S13557
R;Nyitrai, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Seq
A;Reference number: A40997; MUID:92011595; PMID:1917970
A;Accession: A40997
A;Molecule type: mRNA
A;Residues: 1-1938 <NYI>
A;Cross-references: UNIPROT:P24733; GB:X55714; NID:G5611; PIDN:CAA39247.1; PID:G5612
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F;86-763/Domain: myosin motor domain homology <MMOT>
F;176-183/Region: nucleotide-binding motif A (P-loop)
F;547-586/Region: actin-binding #status predicted
F;653-675/Region: actin binding #status predicted
F;836-1938/Domain: coiled coil #status predicted <COI>
F;836-1276/Region: S2
F;1277-1938/Region: light meromyosin
F;182/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted

Query Match 23.6%; Score 123.5; DB 1; Length 1938;
Best Local Similarity 31.3%; Pred. No. 2.7;
Matches 52; Conservative 17; Mismatches 32; Indels 65; Gaps 9;

Qy 1 LEKAE---AELENLLSTLDPGKTQDE---LDKE-AAEALNKKV-EALPNQ----- 44
Db 958 LQAEQDKAHKQNOISTLOEISQDDEHIGKANKKALEANKKTSQDSLOAEDKCNHL 1017

Qy 45 ---VELEELSKLEON-----LKDQETNVEDY---IKEGLEEAI 77
Db 1018 NKLKAKLEQALDELDNLEKRVGVDEKAKRVEQDLASTQENVEDLERVKLEENV 1077

Qy 78 ATKQAE-----LEKTPKELDAALNLELPGDGE 106
Db 1078 RRKEAETSSLNKLDEQNLVSQLQRIKELQARIEL-----EEE 1118

RESULT 5

D71453
hypothetical protein PH0283 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71453
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hainaka, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71453
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-279 <KAW>
A;Cross-references: UNIPROT:O58021; GB:AP000001; NID:G3236128; PIDN:BAA29355.1; PID:G325
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0283

Query Match 23.2%; Score 121.5; DB 2; Length 279;
Best Local Similarity 34.0%; Pred. No. 0.5;
Matches 36; Conservative 19; Mismatches 28; Indels 23; Gaps 4;

Qy 1 LEKAEALNLLSTLDPGKTQDELQKAAEALN-----KKVEALPNQVELEELS 52
Db 164 LEKAKKEIEELKERIETLEKEKELEKESVKLMEYKAKKVE-----ELEKJK 217

Qy 53 KLEDNLKDAETNVEDYIKGLEEAIATKQAELEKTPKELDAALNEL 98
Db 218 EYBEKREIEGRINDY-----EKKI-----RELSEKGLKEKINVL 254

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 17, 2005, 20:04:33 ; Search time 13.853 Seconds
(without alignments)
736.230 Million cell updates/sec

Title: US-10-674-755-22
Perfect score: 523
Sequence: 1 LEKAEAELENLLSTLDPEK.....TPKELDAALNELPGDGEDEE 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 304 | 58.1 | 744 | 2 F95013 | pneumococcal surfa |
| 2 | 194 | 37.1 | 619 | 2 A37887 | surface protein ps |
| 3 | 194 | 37.1 | 619 | 2 A41971 | myosin heavy chain |
| 4 | 123.5 | 23.6 | 1938 | 1 A40997 | hypothetical prote |
| 5 | 121.5 | 23.2 | 279 | 2 D71453 | hypothetical prote |
| 6 | 119 | 22.8 | 281 | 2 F75216 | myosin heavy chain |
| 7 | 117.5 | 22.5 | 2139 | 2 T18296 | myosin heavy chain |
| 8 | 113 | 21.6 | 1940 | 2 A59287 | myosin heavy chain |
| 9 | 112 | 21.4 | 527 | 2 S33068 | myosin heavy chain |
| 10 | 110.5 | 21.1 | 1937 | 2 S38055 | myosin heavy chain |
| 11 | 109 | 20.8 | 1992 | 2 A47297 | myosin heavy chain |
| 12 | 108 | 20.7 | 1269 | 2 F84730 | probable myosin he |
| 13 | 108 | 20.7 | 1961 | 1 A61231 | myosin heavy chain |
| 14 | 106.5 | 20.4 | 1110 | 2 I51116 | NF-180 - sea lampr |
| 15 | 106.5 | 20.4 | 1934 | 2 I48153 | myosin heavy chain |
| 16 | 106 | 20.3 | 1837 | 2 T41023 | probable nuclear p |
| 17 | 105.5 | 20.2 | 858 | 2 S15762 | neurofilament trip |
| 18 | 105.5 | 20.2 | 1964 | 2 A59282 | nonmuscle myosin I |
| 19 | 104.5 | 20.0 | 853 | 2 T51505 | hypothetical prote |
| 20 | 104.5 | 20.0 | 1156 | 2 B70356 | chromosome assembl |
| 21 | 104.5 | 20.0 | 2116 | 2 A26655 | myosin heavy chain |
| 22 | 104 | 19.9 | 577 | 1 A41289 | moesin - human |
| 23 | 104 | 19.9 | 577 | 1 S39804 | moesin - pig |
| 24 | 104 | 19.9 | 1170 | 2 A72287 | hypothetical prote |
| 25 | 104 | 19.9 | 1931 | 2 A59234 | slow myosin heavy |
| 26 | 104 | 19.9 | 1976 | 2 A59252 | myosin heavy chain |
| 27 | 103.5 | 19.8 | 465 | 2 A02986 | myosin alpha heavy |
| 28 | 103.5 | 19.8 | 508 | 2 B72201 | conserved hypothet |
| 29 | 103.5 | 19.8 | 1164 | 2 T24806 | hypothetical prote |

RESULT 1

F95013
pneumococcal surface protein A [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95013
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95013
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <KUR>
A;Cross-references: UNIPROT:Q97T39; GB:A5005672; PIDN:AAK74303.1; PID:g14971584; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0117

Query Match 58.1%; Score 304; DB 2; Length 744;

Best Local Similarity 62.6%; Pred. No. 4.9e-12;

Matches 67; Conservative 14; Mismatches 22; Indels 4; Gaps 2;

Oy 1 LEKAEAELENLLSTLDPEGKTQDELKAEAELENKKVEALPNQV-ELEBEELSKLEENLK 59

Db 346 LAKQTELEKLLDSDPEGKTQDELKAEAELENKKVEALPNQV-ELEBEELSKLEENLK 405

Oy 60 DAETNVEDYIKEGLEAEATKQAELEKTPKELDAALNELPGDGEDEE 106

Db 406 GADSEDD---TAALQNLKATKAELEKTKELDAALNELPGDGEDEE 449

RESULT 2

A97887

surface protein pspA precursor [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: A97887

R;Hoeking, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bursgett, S.; DeHoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A97887

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-619 <KUR>

```
DT 28-OCT-1997 (first entry)
DE Streptococcus pneumoniae PspA central region.
XX
XX PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.
XX
OS Streptococcus pneumoniae; strain Bg7561.
XX
FH Key Location/Qualifiers
FT Misc-difference 44
FT /note= "unidentified amino acid"
XX
FN WO9709994-A1.
XX
PD 20-MAR-1997.
XX
PF 16-SEP-1996; 96WO-US014819.
XX
PR 15-SEP-1995; 95US-00529055.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;
PI Hollingshead S, Tart R, Brooks-Walter A;
XX
XX WPI; 1997-202002/18.
XX
XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
PT in vaccines for protecting animals against S.pneumoniae infection.
XX
XX Example 6; Fig 13; 296pp; English.
XX
XX This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7561.
CC Comparison of the N-terminal and central regions (AAW14533-57 and
CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
CC be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 184 AA;
SQ
Query Match 74.5%; Score 389.5; DB 2; Length 184;
Best Local Similarity 81.3%; Pred. No. 3.6e-25;
Matches 87; Conservative 6; Mismatches 11; Indels 3; Gaps 3;
Oy 2 EKAAELENLLSTDPGKTDQLDKEAAEELNKKVEALPNQV-ELFEELSKLEDNLKD 60
; : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 KKQKNLENLLST-DPGKTDQLDKGAAEELNKKVEALPNVXELEELSPEDNLKD 59
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 61 AETN-VEDYIKEGLEEAATKQAELEKTPKELDAALNELGPDGDEE 106
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 AETNHVEDYIKFEELEEAATKQAELEETPQEVDAALNDLVDPGGEE 106
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: November 17, 2005, 20:19:41
Job time : 76.3256 secs

Db 336 DAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEEE 383

RESULT 13

AAW14590
ID AAW14590 standard; protein; 233 AA.

XX AC AAW14590;
XX 17-OCT-2003 (revised)
DT 28-OCT-1997 (first entry)

XX Streptococcus pneumoniae PspA central region.

DE PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
KW bacteraemia; pneumonia.

XX Streptococcus pneumoniae; strain Ef5668.

OS WO9709994-A1.

PN 20-MAR-1997.

PD 16-SEP-1996; 96WO-US014819.

XX 15-SEP-1995; 95US-00529055.

PF (UABR-) UAB RES FOUND.

PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;

PI Hollingshead S, Tart R, Brooks-Walter A;

XX WPI; 1997-202002/18.

XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used

PT in vaccines for protecting animals against S.pneumoniae infection.

XX Example 6; Fig 13; 296pp; English.

PS This sequence shows the central portion, including the C-terminus of the
CC alpha-helix region and some of the proline-rich region, of pneumococcal
CC surface protein A (PspA) of Streptococcus pneumoniae strain Ef5668 (see
CC also AAW14592). Comparison of the N-terminal and central regions
CC (AAW14533-57 and AAW14562-91) of PspA from different pneumococcal strains
CC can be used to divide the strains into several families based on sequence
CC homologies. PspA polypeptides, or fragments of them, can be used in
CC vaccines to protect animals against S. pneumoniae infection and hence for
CC the prevention of diseases such as otitis media, meningitis, bacteraemia
CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
CC region and the immediate 5' tip of the coding sequence are likely to be
CC the critical sequences for predicting PspA cross-reactions and vaccine
CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 233 AA;

Query Match 85.0%; Score 444.5; DB 2; Length 233;

Best Local Similarity 89.0%; Pred. No. 1.1e-29;

Matches 97; Conservative 4; Mismatches 5; Indels 3; Gaps 3;

QY 1 LEKAAELENLSTLDP-EGKTDQDELKAAEALNKVKEALPNQV-ELEBELSKLEDNL 58

Db 51 LEDAELEKVLATLDPEGKTQDELKAAEALNKVKEALQNVAELEBELSKLEDNL 110

QY 59 KDAET-NVEDYIKGLEEAIATKKALEKTKPKELDAALNELGPDGDEEE 106

Db 111 KDAETNNVEDYIKGLEEAIATKKALEKTKQKELDAALNELGPDGDEEE 159

RESULT 14

ABW02623

ID ABW02623 standard; protein; 185 AA.

XX AC ABW02623;

XX 12-FEB-2004 (first entry)
XX DE Bg7561c pneumococcal surface protein A (PspA) central region.

XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
KW immunological; gene therapy; immunostimulant.
XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 45

FT /label= Unknown

XX US6592876-B1.

XX 15-JUL-2003.

XX 15-SEP-1995; 95US-00529055.

XX 20-APR-1993; 93US-00048896.

XX 06-JUN-1995; 95US-00465746.

XX (UABR-) UAB RES FOUND.

XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX WPI; 2003-862841/80.

XX Immunological composition for obtaining expression products used for
PT detecting the presence of Streptococcus pneumoniae or its strain,
PT comprises at least two different full length isolated gene encoding
PT pneumococcal surface protein A.
XX Example 6; SEQ ID NO 69; 121pp; English.
PS The present invention relates to an immunological composition comprising
CC at least 2 different full length isolated genes encoding pneumococcal
CC surface protein A (PspAa) from different groups based on restriction
CC fragment polymorphism analysis. The invention is useful for obtaining
CC expression products by recombinant techniques to detect, determine,
CC isolate or diagnose the presence of Streptococcus pneumoniae or its
CC strain. The expression product is useful for preparing antibodies, an
CC immunological or vaccine compositions, for eliciting antibodies, an
CC immunological response (other than or additional to antibodies) or a
CC protective response (including antibody or other immunological response
CC by administering compositions to a host). The invention is also useful as
CC vaccines and in gene therapy. The present sequence is Bg7561c
CC pneumococcal surface protein A (PspA) central region. This sequence is
XX used in the exemplification of the invention

XX SQ Sequence 185 AA;

Query Match 79.0%; Score 413; DB 7; Length 185;

Best Local Similarity 83.2%; Pred. No. 3.8e-27;

Matches 89; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

QY 2 EKAAELENLSTLDP-EGKTDQDELKAAEALNKVKEALPNQV-ELEBELSKLEDNLKD 60

Db 1 KKQKVNLENLSTLDP-EGKTDQDELKAAEALNKVKEALPNVXELEBELSPEDNLKD 60

QY 61 AETN-VEDYIKGLEEAIATKKALEKTKPKELDAALNELGPDGDEEE 106

Db 61 AETHNVEDYIKGLEEAIATKKALEETPQEVDAALNDLVPDGGDEEE 107

RESULT 15

AAW14589

ID AAW14589 standard; protein; 184 AA.

XX AC AAW14589;

XX 17-OCT-2003 (revised)


```
Qy      1 LEKAAELENLLSTLDPEGKTQDELDEKAAAELNKKVEALPNQV -ELEEEESLKLEENLTK 59
```

WPI; 2004-192068/18.

DR XX
XX XX
PT Treating Streptococcus pneumoniae infection in a subject lacking a
PT functional spleen comprises administering an antibody that recognizes
PT pneumococcal surface protein A (PspA) or its binding portion.

XX XX
XX Claim 17; SEQ ID NO 2; 41pp; English.

XX XX
XX The present invention relates to treating Streptococcus pneumoniae
CC infection in a subject lacking a functional spleen comprises
CC administering an antibody that recognizes pneumococcal surface protein A
CC (PspA) or its binding portion. The method is useful for treating or
CC preventing Streptococcus pneumoniae infection in a subject lacking a
CC functional spleen. The disease-associated injury is especially due to
CC hemolytic anemia disease, leukemia or lymphoma, especially sickle cell
CC anemia or Hodgkin's disease. The present sequence represents the alpha
CC helical region PspA molecule from the Rx1 strain of Streptococcus
CC pneumoniae.

XX XX
XX Sequence 369 AA;

| | Query Match | 87.0% | Score 455; | DB 8; | Length 369; |
|----|-----------------------|---|--------------------|-----------|-------------|
| | Best Local Similarity | 89.8%; | Pred. No. 2.3e-30; | | |
| | Matches 97; | Conservative 4; | Mismatches 5; | Indels 2; | Gaps 2; |
| Qy | 1 | LEKAAELENLSTLDPEGKTQDDELDKAAEAAELNKKVEALPNQV-ELEELSLEDNLK | 59 | | |
| | | : : : : : : : : : : | | | |
| Db | 245 | LEDAELEKVLATLDPEGKTQDDELDKAAEAAELNKKVEALQNVAAELEELSLEDNLK | 304 | | |
| Qy | 60 | DAET-NVEDYIKGLEIAIATKQAELEKTPKELDAALNELGPDGDEE | 106 | | |
| Db | 305 | DAETNNVEDYIKGLEIAIATKKALEKTKQELDAALNELGPDGDEE | 352 | | |

| | |
|----------|---|
| RESULT 9 | |
| AAW14592 | |
| ID | AAW14592 standard; protein; 458 AA. |
| XX | |
| AC | AAW14592; |
| XX | |
| DT | 17-OCT-2003 (revised) |
| DT | 27-OCT-1997 (first entry) |
| XX | |
| XX | Streptococcus pneumoniae PspA surface protein. |
| XX | |
| KW | PspA; pneumococcal surface protein; vaccine; otitis media; meningitis; |
| KW | bacteraemia; pneumonia. |
| XX | |
| OS | Streptococcus pneumoniae; strain Ef5668. |
| XX | |
| PN | WO9709994-A1. |
| XX | |
| PD | 20-MAR-1997. |
| XX | |
| PF | 16-SEP-1996; 96WO-US014819. |
| XX | |
| PR | 15-SEP-1995; 95US-00529055. |
| XX | |
| PA | (UABR-) UAB RES FOUND. |
| XX | |
| PI | Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain WJ; |
| PI | Hollingshead S, Tart R, Brooks-Walter A; |
| XX | |
| DR | WPI; 1997-202002/18. |
| DR | N-PSDB; AAT61724. |
| XX | |
| PT | Streptococcus pneumoniae surface protein PspC and truncated PspA - used |
| PT | in vaccines for protecting animals against S.pneumoniae infection. |
| XX | |
| PS | Disclosure; Fig 13; 296pp; English. |
| XX | |
| CC | This sequence comprises the pneumococcal surface protein A (pspA) of |
| CC | Streptococcus pneumoniae strain Ef5668. The sequence was deduced from the |

| | |
|-----------|--|
| CC | pspA gene (AAT61724). PspA polypeptides, or fragments of them, can be |
| CC | used in vaccines to protect animals against <i>S. pneumoniae</i> infection and |
| CC | hence for the prevention of diseases such as otitis media, meningitis, |
| CC | bacteraemia and pneumonia. (Updated on 17-OCT-2003 to standardise OS |
| CC | field) |
| XX | |
| SQ | Sequence 458 AA; |
| | Query Match 87.0%; Score 455; DB 2; Length 458; |
| | Best Local Similarity 89.8%; Pred. No. 3e-30; |
| | Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2 |
| Qy | 1 LEKAEALENLSTLDPEGTQDELDKAEAAELNKKVEALPNQV-ELEELSLEDNLK 59 |
| Db | 276 LEDAELELEKVLATLDPEGTQDELDKAEAAELNKKVEALQNVAELEELSLEDNLK 335 |
| Qy | 60 DAST-NVEDYIKGLEIAIAIKQAELEKTKPKELDAALNELGPDGDEE 106 |
| Db | 336 DASTNNVEDYIKGLEIAIAIKQAELEKTKPKELDAALNELGPDGDEE 383 |
| RESULT 10 | |
| ABW02626 | |
| ID | ABW02626 standard; protein; 458 AA. |
| XX | AC ABW02626; |
| XX | AC |
| DT | 12-FEB-2004 (first entry) |
| XX | |
| DE | EF5668 pneumococcal surface protein A (PspA). |
| XX | |
| KW | Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine; |
| KW | immunological; gene therapy; immunostimulant. |
| OS | Unidentified. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | Misc-difference 458 |
| FT | /note= "Encoded by GC" |
| XX | |
| PN | US6592876-B1. |
| XX | |
| PD | 15-JUL-2003. |
| XX | |
| PF | 15-SEP-1995; 95US-00529055. |
| XX | |
| PR | 20-APR-1993; 93US-00048896. |
| XX | |
| PR | 06-JUN-1995; 95US-00465746. |
| XX | |
| PA | (UABR-) UAB RES FOUND. |
| XX | |
| PI | Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A; |
| XX | |
| DR | WPI; 2003-862841/80. |
| DR | N-PSDB; AAD64535. |
| XX | |
| PT | Immunological composition for obtaining expression products used for |
| PT | detecting the presence of <i>Streptococcus pneumoniae</i> or its strain, |
| PT | comprises at least two different full length isolated gene encoding |
| PT | pneumococcal surface protein A. |
| XX | |
| PS | Example 6; SEQ ID NO 73; 121pp; English. |
| XX | |
| CC | The present invention relates to an immunological composition comprising |
| CC | at least 2 different full length isolated genes encoding pneumococcal |
| CC | surface protein A (PspAs) from different groups based on restriction |
| CC | fragment polymorphism analysis. The invention is useful for obtaining |
| CC | expression products by recombinant techniques to detect, determine, |
| CC | isolate or diagnose the presence of <i>Streptococcus pneumoniae</i> or its |
| CC | strain. The expression product is useful for preparing antigenic, |
| CC | immunological or vaccine compositions, for eliciting antibodies, an |
| CC | immunological response (other than or additional to antibodies) or a |
| CC | protective response (including antibody or other immunological response |

XX Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
 KW immunological; gene therapy; immunostimulant.

XX Unidentified.

XX US6592876-B1.

XX 15-JUL-2003.

XX 15-SEP-1995; 95US-00529055.

XX 20-APR-1993; 93US-00048896.

XX 06-JUN-1995; 95US-00465746.

XX (UABR-) UAB RES FOUND.

XX Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX WPI; 2003-862841/80.

XX Immunological composition for obtaining expression products used for
 PT detecting the presence of Streptococcus pneumoniae or its strain,
 PT comprises at least two different full length isolated gene encoding
 PT pneumococcal surface protein A.

XX Example 6; SEQ ID NO 70; 121pp; English.

XX The present invention relates to an immunological composition comprising
 CC at least 2 different full length isolated genes encoding pneumococcal
 CC surface protein A (PspA) from different groups based on restriction
 CC fragment polymorphism analysis. The invention is useful for obtaining
 CC expression products by recombinant techniques to detect, determine,
 CC isolate or diagnose the presence of Streptococcus pneumoniae or its
 CC strain. The expression product is useful for preparing antigenic,
 CC immunological or vaccine compositions, for eliciting antibodies, an
 CC immunological response (other than or additional to antibodies) or a
 CC protective response (including antibody or other immunological response
 CC by administering compositions to a host). The invention is also useful as
 CC vaccines and in gene therapy. The present sequence is Ef5668c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention

XX Sequence 232 AA;

Query Match 87.0%; Score 455; DB 7; Length 232;
 Best Local Similarity 89.8%; Pred. No. 1.4e-30;
 Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAELENLLSTLDPEGKTQDELKAEAAEALNKKVEALPNQV-ELEBEELSKLEDNLK 59

Db 51 LEDAELEKLVATLDPEGKTQDELKAEAAEALNKKVEALQNVQVAEELSKLEDNLK 110

Qy 60 DAET-NVEDYIKEGLEAAIAATKQAELEKTPKELDAALNELGPDGDEE 106

Db 111 DAETNNVEDYIKEGLEAAIAATKQAELEKTPKELDAALNELGPDGDEE 158

RESULT 7

AD052055

ID AD052055 standard; protein; 275 AA.

XX AD052055;

XX 12-AUG-2004 (first entry)

XX S. pneumoniae strain EF5688 PspA alpha helical domain.

XX Immunogenic composition; vaccine; Th2-type immune response ;

Kw pneumococcal surface protein A; PspA.

OS Streptococcus pneumoniae.

XX

PN US2004101531-A1.

XX 27-MAY-2004.

XX 15-APR-2003; 2003US-00414532.

XX 16-APR-2002; 2002US-0372710P.

XX (CURT/) CURTISS R.

XX (KANG/) KANG H Y.

XX Curtiss R, Kang HY;

XX WPI; 2004-399655/37.

XX New vaccine comprising a live attenuated strain of pathogenic gram-
 PT negative bacteria, useful in eliciting a Th2-type immune response in a
 PT vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
 PT or bacteria.

XX Claim 17; SEQ ID NO 1; 94pp; English.

XX The invention relates to immunogenic compositions and vaccines comprising
 CC a live attenuated strain of pathogenic gram negative bacteria that
 CC secretes an antigen. The vaccine is useful in eliciting a Th2-type immune
 CC response in a vertebrate against pathogens, e.g., helminths, fungi,
 CC viruses, protozoans or bacteria. The present sequence is Streptococcus
 CC pneumoniae strain EF5688 pneumococcal surface protein A (PspA) alpha
 CC helical domain. This sequence is used in the invention.

XX Sequence 275 AA;

Query Match 87.0%; Score 455; DB 8; Length 275;

Best Local Similarity 89.8%; Pred. No. 1.7e-30;

Matches 97; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Qy 1 LEKAELENLLSTLDPEGKTQDELKAEAAEALNKKVEALPNQV-ELEBEELSKLEDNLK 59

Db 167 LEDAELEKLVATLDPEGKTQDELKAEAAEALNKKVEALQNVQVAEELSKLEDNLK 226

Qy 60 DAET-NVEDYIKEGLEAAIAATKQAELEKTPKELDAALNELGPDGDEE 106

Db 227 DAETNNVEDYIKEGLEAAIAATKQAELEKTPKELDAALNELGPDGDEE 274

RESULT 8

ADK32496

ID ADK32496 standard; protein; 369 AA.

XX ADK32496;

XX 20-MAY-2004 (first entry)

XX alpha helical region PspA molecule from the Rx1 strain.

XX Streptococcus pneumoniae infection; pneumococcal surface protein A; PspA;
 KW hemolytic anemia disease; leukemia; lymphoma; sickle cell anemia;
 KW Hodgkin's disease.

XX Streptococcus pneumoniae.

XX WO2004016231-A2.

XX 26-FEB-2004.

XX 17-FEB-2003; 2003WO-US008199.

XX 15-MAR-2002; 2002US-0365351P.

XX (UABR-) UAB RES FOUND.

XX Briles DE;

XX

QY 60 DAET-NVEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 106
|||||
Db 8041 DAETNNVEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 8088

RESULT 4

AAW14588
ID AAW14588 standard; protein; 212 AA.

XX AC AAW14588;

XX DT 17-OCT-2003 (revised)
XX DT 28-OCT-1997 (first entry)

XX DE Streptococcus pneumoniae PspA central region.

XX KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
XX KW bacteraemia; pneumonia.

XX OS Streptococcus pneumoniae; strain Bg7817.

XX PN WO9709994-A1.

XX PD 20-MAR-1997.

XX PF 16-SEP-1996; 96WO-US014819.

XX PR 15-SEP-1995; 95US-00529055.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Crain MJ;

XX PI Hollingshead S, Tart R, Brooks-Walter A;

XX DR WPI; 1997-202002/18.

XX ST Streptococcus pneumoniae surface protein PspC and truncated PspA - used
XX PT in vaccines for protecting animals against S.pneumoniae infection.

XX PS Example 6; Fig 13; 296pp; English.

XX CC This sequence shows the central portion, including the C-terminus of the
XX CC alpha-helix region and some of the proline-rich region, of pneumococcal
XX CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg7817.
XX CC Comparison of the N-terminal and central regions (AAW14533-57 and
XX CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
XX CC be used to divide the strains into several families based on sequence
XX CC homologies. PspA polypeptides, or fragments of them, can be used in
XX CC vaccines to protect animals against S. pneumoniae infection and hence for
XX CC the prevention of diseases such as otitis media, meningitis, bacteraemia
XX CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
XX CC region and the immediate 5' tip of the coding sequence are likely to be
XX CC the critical sequences for predicting PspA cross-reactions and vaccine
XX CC composition. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 212 AA;

Query Match 92.0%; Score 481; DB 2; Length 212;
Best Local Similarity 95.4%; Pred. No. 7.8e-33;
Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59
|||||
Db 28 LEKAGAGLNLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-AELEEELSKLEDNLK 87

QY 60 DAETN-VEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 106
|||||
Db 88 DAETNHVEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 135

RESULT 5

ABW02622
ID ABW02622 standard; protein; 212 AA.

XX ABW02622;
XX DT 12-FEB-2004 (first entry)
XX DE Bg7817c pneumococcal surface protein A (PspA) central region.
XX KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
XX KW immunological; gene therapy; immunostimulant.

XX OS Unidentified.

XX PN US6592876-B1.

XX PD 15-JUL-2003.

XX PF 15-SEP-1995; 95US-00529055.

XX PR 20-APR-1993; 93US-00048896.

XX PR 06-JUN-1995; 95US-00465746.

XX PA (UABR-) UAB RES FOUND.

XX PI Briles DE, McDaniel LS, Swiatlo E, Yother J, Brooks-Walter A;

XX DR WPI; 2003-862841/80.

XX PT Immunological composition for obtaining expression products used for
XX PT detecting the presence of Streptococcus pneumoniae or its strain,
XX PT comprises at least two different full length isolated gene encoding
XX PT pneumococcal surface protein A.

XX PS Example 6; SEQ ID NO 68; 121pp; English.

XX CC The present invention relates to an immunological composition comprising
XX CC at least 2 different full length isolated genes encoding pneumococcal
XX CC surface protein A (PspAs) from different groups based on restriction
XX CC fragment polymorphism analysis. The invention is useful for obtaining
XX CC expression products by recombinant techniques to detect, determine,
XX CC isolate or diagnose the presence of Streptococcus pneumoniae or its
XX CC strain. The expression product is useful for preparing antigenic,
XX CC immunological or vaccine compositions, for eliciting antibodies, an
XX CC immunological response (other than or additional to antibodies) or a
XX CC protective response (including antibody or other immunological response
XX CC by administering compositions to a host). The invention is also useful as
XX CC vaccines and in gene therapy. The present sequence is Bg7817c
XX CC pneumococcal surface protein A (PspA) central region. This sequence is
XX CC used in the exemplification of the invention

XX SQ Sequence 212 AA;

Query Match 92.0%; Score 481; DB 7; Length 212;
Best Local Similarity 95.4%; Pred. No. 7.8e-33;
Matches 103; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 LEKAAELENLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-ELEEEELSKLEDNLK 59
|||||
Db 28 LEKAGAGLNLSTLDPEGKTQDELDKAAAEALNKKVEALPNQV-AELEEELSKLEDNLK 87

QY 60 DAETN-VEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 106
|||||
Db 88 DAETNHVEDYIKEGLEEAIAATQAELEKTPKELDAALNELGPDGDEEE 135

RESULT 6

ABW02624
ID ABW02624 standard; protein; 232 AA.

XX AC ABW02624;

XX DT 12-FEB-2004 (first entry)

XX DE Efs668c pneumococcal surface protein A (PspA) central region.

CC vaccines and in gene therapy. The present sequence is Bg11703c
 CC pneumococcal surface protein A (PspA) central region. This sequence is
 CC used in the exemplification of the invention
 XX Sequence 211 AA;
 SQ

Query Match 96.0%; Score 502; DB 7; Length 211;
 Best Local Similarity 98.1%; Pred. No. 1.3e-34;
 Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 |||||
 Db 25 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQVSELEEELSKLEDNLK 84
 |||||

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 106
 |||||
 Db 85 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 132
 |||||

RESULT 2
 AAW14587
 ID AAW14587 standard; protein; 238 AA.
 XX
 AC AAW14587;
 XX
 DT 17-OCT-2003 (revised)
 DT 28-OCT-1997 (first entry)
 XX
 DE Streptococcus pneumoniae PspA central region.
 XX
 KW PspA; pneumococcal surface protein; vaccine; otitis media; meningitis;
 KW bacteraemia; pneumonia.
 XX
 OS Streptococcus pneumoniae; strain Bg11703.
 XX
 PN WO9709994-A1.
 XX
 PD 20-MAR-1997.
 XX
 PF 16-SEP-1996; 96WO-US014819.
 XX
 PR 15-SEP-1995; 95US-00529055.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 PI WPI; 1997-202002/18.
 DR
 XX Streptococcus pneumoniae surface protein PspC and truncated PspA - used
 PT in vaccines for protecting animals against S.pneumoniae infection.
 XX
 PS Example 6; Fig 13; 296pp; English.
 XX

This sequence shows the central portion, including the C-terminus of the
 CC alpha-helix region and some of the proline-rich region, of pneumococcal
 CC surface protein A (PspA) of Streptococcus pneumoniae strain Bg11703.
 CC Comparison of the N-terminal and central regions (AAW14533-57 and
 CC AAW14562-91) of PspA polypeptides from different pneumococcal strains can
 CC be used to divide the strains into several families based on sequence
 CC homologies. PspA polypeptides, or fragments of them, can be used in
 CC vaccines to protect animals against S. pneumoniae infection and hence for
 CC the prevention of diseases such as otitis media, meningitis, bacteraemia
 CC and pneumonia. The sequence of the 3' half of the PspA alpha-helical
 CC region and the immediate 5' tip of the coding sequence are likely to be
 CC the critical sequences for predicting PspA cross-reactions and vaccine
 CC composition. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 238 AA;

Query Match 96.0%; Score 502; DB 2; Length 238;
 Best Local Similarity 98.1%; Pred. No. 1.5e-34;

Qy 1 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 |||||
 Db 7981 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQVSELEEELSKLEDNLK 8040
 |||||

Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 |||||
 Db 25 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQVSELEEELSKLEDNLK 84
 |||||

Qy 60 DAET-NVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 106
 |||||
 Db 85 DAETNNVEDYIKGLEEAIATKQAELEKTPKELDAALNELGPDGDEE 132
 |||||

RESULT 3
 ABU08487
 ID ABU08487 standard; protein; 8991 AA.
 XX
 AC ABU08487;
 XX
 DT 24-JUN-2003 (first entry)
 XX
 DE S. pneumoniae pneumococcal surface protein A (PspA) protein.
 XX
 KW Pneumococcal surface protein C; PspC; pneumococcal surface protein A;
 KW alpha-helical; proline rich; repeat region; pneumococcal infection; PspA;
 KW antibacterial.
 XX
 OS Streptococcus pneumoniae.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 1..8991
 FT /note= "All Xaa residues within this sequence are
 FT unknown"
 XX
 PN US6500613-B1.
 XX
 PD 31-DEC-2002.
 XX
 PF 16-SEP-1996; 96US-0071741.
 XX
 PR 15-SEP-1995; 95US-00529055.
 XX
 PA (UYAL-) UNIV ALABAMA.
 XX
 PI Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Crain MJ;
 PI Hollingshead S, Tart R, Brooks-Walter A;
 PI WPI; 2003-361534/34.
 DR
 XX Isolated PspC amino acid sequence used as polymerase chain reaction or
 PT hybridization probe, comprises pneumococcal surface protein having alpha-
 PT helical, proline rich and repeat regions.
 XX
 PS Disclosure; Col 145-188; 186pp; English.
 XX
 CC The present invention relates to the isolation of Streptococcus
 CC pneumoniae pneumococcal surface protein C (PspC), and the polynucleotide
 CC sequence encoding it. PspC is a pneumococcal surface protein A (PspA)-
 CC like protein having alpha-helical, proline rich and repeat regions. The
 CC PspC and PspA proteins may be used in a vaccine to protect against
 CC pneumococcal infections. The polynucleotide sequences encoding PspC and
 CC PspA may be used for the expression of the proteins, and as PCR primers
 CC or hybridisation probes. The present sequence represents S. pneumoniae
 CC PspA protein
 XX
 SQ Sequence 8991 AA;

Query Match 96.0%; Score 502; DB 6; Length 8991;
 Best Local Similarity 98.1%; Pred. No. 9.9e-33;
 Matches 106; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQV-ELEEELSKLEDNLK 59
 |||||
 Db 7981 LEKAAELENLLSTLDPGKQTQDELKAAAEALNKKVEALPNQVSELEEELSKLEDNLK 8040
 |||||

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OM protein - protein search, using sw model

Run on: November 17, 2005, 19:20:59 ; Search time 75.3256 Seconds
(without alignments)
544.259 Million cell updates/sec

Title: US-10-674-755-22
Perfect score: 523
Sequence: 1 LEKAEAELENLSTLDPEKG.....TPKELDAALNELGPDGDEE 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 502 | 96.0 | 211 | 7 | ABW02621 |
| 2 | 502 | 96.0 | 238 | 2 | AAW14587 |
| 3 | 502 | 96.0 | 8991 | 6 | ABU08487 |
| 4 | 481 | 92.0 | 212 | 2 | AAW14588 |
| 5 | 481 | 92.0 | 212 | 7 | ABW02622 |
| 6 | 455 | 87.0 | 232 | 7 | ABW02624 |
| 7 | 455 | 87.0 | 275 | 8 | ADO52055 |
| 8 | 455 | 87.0 | 369 | 8 | ADK52496 |
| 9 | 455 | 87.0 | 458 | 2 | AAW14592 |
| 10 | 455 | 87.0 | 458 | 7 | ABW02626 |
| 11 | 455 | 87.0 | 653 | 8 | ADK52495 |
| 12 | 455 | 87.0 | 653 | 8 | ADO52080 |
| 13 | 444.5 | 85.0 | 233 | 2 | AAW14590 |
| 14 | 413 | 79.0 | 185 | 7 | ABW02623 |
| 15 | 389.5 | 74.5 | 184 | 2 | AAW14589 |
| 16 | 315 | 60.2 | 213 | 7 | ABW02601 |
| 17 | 304 | 58.1 | 213 | 2 | AAW14567 |
| 18 | 304 | 58.1 | 416 | 8 | ADK52498 |
| 19 | 304 | 58.1 | 526 | 8 | ADK52497 |
| 20 | 304 | 58.1 | 744 | 6 | ABU00449 |
| 21 | 304 | 58.1 | 744 | 8 | ADM92054 |
| 22 | 304 | 58.1 | 745 | 3 | AAW81652 |
| 23 | 303 | 57.9 | 641 | 2 | AAW61217 |
| 24 | 303 | 57.9 | 641 | 5 | ABP54636 |
| 25 | 303 | 57.9 | 641 | 7 | ADC45241 |

| | | | | | | | | |
|----|-------|------|-----|---|----------|----------|-----------|---------|
| 26 | 300 | 57.4 | 197 | 7 | ABW02598 | Abw02598 | Ac122c | pn |
| 27 | 296.5 | 56.7 | 459 | 8 | ADO15316 | Ado15316 | S | pneumon |
| 28 | 282.5 | 54.0 | 196 | 2 | AAW14564 | Aaw14564 | Streptoco | |
| 29 | 275 | 52.6 | 233 | 7 | ABW02606 | Abw02606 | Bf1019c | p |
| 30 | 272 | 52.0 | 487 | 8 | ADR04321 | Adr04321 | Streptoco | |
| 31 | 272 | 52.0 | 489 | 8 | ADO52088 | Ado52088 | Streptoco | |
| 32 | 272 | 52.0 | 524 | 8 | ADO52082 | Ado52082 | E. coli | B |
| 33 | 272 | 52.0 | 627 | 8 | ADO52129 | Ado52129 | E. coli | B |
| 34 | 268 | 51.2 | 233 | 2 | AAW14572 | Aaw14572 | Streptoco | |
| 35 | 262.5 | 50.2 | 290 | 8 | ADO52119 | Ado52119 | pYA3637 | b |
| 36 | 262.5 | 50.2 | 298 | 8 | ADO52127 | Ado52127 | pYA3637 | b |
| 37 | 260.5 | 49.8 | 230 | 8 | ADO52086 | Ado52086 | S. pneumo | |
| 38 | 260.5 | 49.8 | 230 | 8 | ADR04319 | Adr04319 | Streptoco | |
| 39 | 257.5 | 49.2 | 119 | 2 | AAW46291 | Aaw46291 | Pneumococ | |
| 40 | 257.5 | 49.2 | 215 | 2 | AAW14563 | Aaw14563 | Streptoco | |
| 41 | 257.5 | 49.2 | 215 | 7 | ABW02597 | Abw02597 | Atcc6303c | |
| 42 | 194 | 37.1 | 319 | 2 | AAW04375 | Aaw04375 | Streptoco | |
| 43 | 194 | 37.1 | 619 | 2 | AAW63437 | Aaw63437 | Pneumococ | |
| 44 | 194 | 37.1 | 619 | 2 | AAW87598 | Aaw87598 | Pneumococ | |
| 45 | 194 | 37.1 | 619 | 2 | AAW86911 | Aaw86911 | Pneumococ | |

ALIGNMENTS

RESULT 1
ABW02621
ID ABW02621 standard; protein; 211 AA.
XX AC ABW02621;
XX DT 12-FEB-2004 (first entry)
XX DE Bg11703c pneumococcal surface protein A (PspA) central region.
XX KW Pneumococcal surface protein A; PspA; diagnosis; antigenic; vaccine;
XX KW immunological; gene therapy; immunostimulant.
XX OS Unidentified.
XX PN US592876-B1.
XX PD 15-JUL-2003.
XX PF 15-SEP-1995; 95US-00529055.
XX PR 20-APR-1993; 93US-00048896.
XX PR 06-JUN-1995; 95US-00465746.
XX (UABR-) UAB RES FOUND.
XX Briles DE, Mcdaniel LS, Swiatlo E, Yother J, Brooks-Walter A;
XX WPI; 2003-862841/80.
XX Immunological composition for obtaining expression products used for
XX detecting the presence of Streptococcus pneumoniae or its strain,
XX comprises at least two different full length isolated gene encoding
XX pneumococcal surface protein A.
XX Example 6; SEQ ID NO 67; 121bp; English.
XX The present invention relates to an immunological composition comprising
XX at least 2 different full length isolated genes encoding pneumococcal
XX surface protein A (PspAs) from different groups based on restriction
XX fragment polymorphism analysis. The invention is useful for obtaining
XX expression products by recombinant techniques to detect, determine,
XX isolate or diagnose the presence of Streptococcus pneumoniae or its
XX strain. The expression product is useful for preparing antigenic,
XX immunological or vaccine compositions, for eliciting antibodies, an
XX immunological response (other than or additional to antibodies) or a
XX protective response (including antibody or other immunological response
XX by administering compositions to a host). The invention is also useful as